

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 21, 2004, 08:36:24 ; Search time 21 Seconds  
(without alignments)  
41.215 Million cell updates/sec

Title: US-09-625-963A-1

Perfect score: 51

Sequence: 1 RMPFNAPYL 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	51	100.0	410	2	JC5046	Wlms' tumor suppr
2	51	100.0	448	2	S33926	Wlms' tumor prote
3	51	100.0	449	2	A38080	Wlms' tumor suscep
4	51	100.0	449	2	A39692	Wlms' tumor prote
5	41	80.4	213	2	AD1343	hypothetical prote
6	41	80.4	213	2	AH1713	hypothetical prote
7	40	78.4	262	1	G64144	hypothetical prote
8	39	76.5	203	2	C71375	conserved hypochet
9	38	74.5	205	2	F83495	probable hydrolase
10	38	74.5	214	2	AB2195	serine esterase [i
11	38	74.5	581	2	E86408	PTH9, 11 protein -
12	37	72.5	466	2	S42210	ISG-34K protein -
13	37	72.5	854	2	S33558	unc-33 protein - C
14	37	72.5	1232	2	A55478	neuronal apoptosis
15	36	70.6	85	2	S17463	glutathione transf
16	36	70.6	115	2	S39393	glutathione transf
17	36	70.6	142	2	S17462	glutathione transf
18	36	70.6	217	2	JX0095	glutathione transf
19	36	70.6	218	1	XURIG4	glutathione transf
20	36	70.6	218	1	B34159	glutathione transf
21	36	70.6	218	2	A29036	glutathione transf
22	36	70.6	218	2	S13202	glutathione transf
23	36	70.6	218	2	S33860	glutathione transf
24	36	70.6	218	2	A46143	mu-class glutathio
25	36	70.6	218	2	A23732	glutathione transf
26	36	70.6	218	2	A39375	glutathione transf
27	36	70.6	218	2	S32425	glutathione transf
28	36	70.6	218	2	A46048	glutathione transf
29	36	70.6	218	2	S01719	glutathione transf

30	36	70.6	218	2	B28946	glutathione transf
31	36	70.6	218	2	A29794	glutathione transf
32	36	70.6	218	2	A47486	glutathione transf
33	36	70.6	218	2	S65674	glutathione transf
34	36	70.6	220	2	S18464	glutathione transf
35	36	70.6	225	2	A35295	glutathione transf
36	36	70.6	284	2	F95120	hydroxylase, probabl
37	36	70.6	284	2	B97990	conserved hypochet
38	36	70.6	358	2	JC5964	apoptosis inhibito
39	36	70.6	381	2	S65212	hypothetical prote
40	36	70.6	382	2	A48492	polyaccharide exp
41	36	70.6	432	2	B96515	hypothetical prote
42	36	70.6	434	2	C96515	hypothetical prote
43	36	70.6	487	2	T07960	probable (S)-N-met
44	36	70.6	487	2	T07963	probable (S)-N-met
45	36	70.6	618	2	S68450	apoptosis inhibito

#### ALIGNMENTS

##### RESULT 1

JC5046 Wlms' tumor suppressor protein - African clawed frog

N:Alternate names: WTI

C:Species: Xenopus laevis (African clawed frog)

C>Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 31-Jan-1997

C/Accession: JC5046

R/Semba, K.; Salto-Ueno, R.; Takayama, G.; Kondo, M.

Gene 175, 167-172, 1996

A:Title: cDNA cloning and its proneurophos-specific expression of the Wlms' tumor suppress

A:Reference number: JC5046; MID:97074667; PMID:8917094

A:Content: testis

A:Accession: JC5046

A:Molecule type: mRNA

A:Residues: 1-410 <SSM>

A:Cross-references: DDBJ:DB2051

C:Comment: This protein is involved in kidney morphogenesis.

C:Genetics:

A:Gene: wtl

Query Match 100.0%; Score 51; DB 2; Length 410;

Best Local Similarity 100.0%; Pred. No. 0.049; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9

Db 107 RMPFNAPYL 115

##### RESULT 2

S33926 Wlms' tumor protein WTI - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 10-May-1996

C/Accession: S33926

R/Sharma, P.M.; Yang, X.; Bowman, M.; Roberts, V.; Sukumar, S.

Cancer Res. 52, 6407-6412, 1992

A:Title: Molecular cloning of rat Wlms' tumor complementary DNA and a study of messenger

A:Reference number: S33926; MID:93046155; PMID:1330293

A:Accession: S33926

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-448 <SHA>

A:Cross-references: EMBL:X69716

C:Genetics:

A:Gene: WTI

C:Keywords: tumor suppressor

Query Match 100.0%; Score 51; DB 2; Length 448;

Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
 |||||  
 Db 125 RMFPNAPYL 133

RESULT 3

A:Gene: GDB:WT1  
 A:Cross-references: GDB:120496; OMIM:194070  
 A:Map position: 11p13-11p13  
 A:Insertions: 148/1, 189/1, 223/2, 249/2, 266/2, 298/3, 349/1, 379/1, 410/1  
 A:Note: mRNA transcripts containing both alternatively spliced regions are the most abundant  
 C:Keywords: alternative splicing; DNA binding; kidney; tumor suppressor; zinc finger  
 F:1-407/411-449/Product: Wilms tumor susceptibility protein WT1, splice form 1 #status predicted  
 F:1-249/267-449/Product: Wilms tumor susceptibility protein WT1, splice form 2 #status predicted  
 F:1-249/267-407/411-449/Product: Wilms tumor susceptibility protein WT1, splice form 3 #status predicted

A:Accession: A38080; S08273; A34673; I38504; I52811; I58315; A56411; S26286  
 C:Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 20-Jun-2000  
 A:Species: Homo sapiens (man)  
 A:Title: The genomic organization and expression of the WT1 gene.  
 A:Reference number: A38080; PMID:92241883; PMID:1572653  
 A:Accession: A38080  
 A:Molecule type: DNA  
 A:Residues: 1-449 <G851>  
 A:Cross-references: GB:X61631; GB:S99414; NID:937981; PIDN:CAA43819.1; PID:9825731  
 A:Note: It is uncertain whether Met-1 is the initiator or whether translation is initiated  
 A:Note: sequence extracted from NCBI backbone (NCBIN:99414, NCBIN:99422, NCBIN:99479, NC  
 A:Note: the sequence in Genbank entry HSMWGEX1, release 113.0, PIDN:CAA43819.1 differs  
 R:Gessler, M.; Kontig, A.; Bruns, G.A.  
 Genomics 12, 807-813, 1992  
 A:Title: Isolation and characterization of a zinc finger polypeptide gene at the human  
 A:Reference number: S08273; PMID:90158822; PMID:2154702  
 A:Accession: S08273  
 A:Molecule type: mRNA  
 A:Residues: 'SRHRPHRACPLRPTSPPTGPAAGTAQAGPRLLALIDFLDQDASTCVPAPASQHT  
 A:Cross-references: EMBL:X51630; NID:937977; PIDN:CAA35956.1; PID:937978  
 R:Call, K.M.; Glaeser, T.; Ito, C.Y.; Buckler, A.O.; Pelletier, J.; Haber, D.A.; Rose, E.  
 Cell 60, 509-520, 1990  
 A:Title: Isolation and characterization of a zinc finger polypeptide gene at the human  
 A:Reference number: A34673; PMID:90150277; PMID:2154335  
 A:Accession: A34673  
 A:Molecule type: mRNA  
 A:Residues: 85-249, 267-364, 'F', 366-386, 'T', 388-407, 411-449 <CAL>  
 A:Cross-references: GB:M30393; NID:9340381; PIDN:AAA6810.1; PID:9340382  
 R:Haber, D.A.; Sohn, R.L.; Buckler, A.O.; Pelletier, J.; Call, K.M.; Housman, D.E.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 9618-9622, 1991  
 A:Title: Alternative splicing and genomic structure of the Wilms tumor gene WT1.  
 A:Reference number: A56411; PMID:92052142; PMID:1658787  
 A:Contents: annotation; alternative splicing  
 R:Phealan, S.A.; Lindberg, C.; Call, K.M.  
 Cell Growth Differ. 5, 677-686, 1994  
 A:Title: Wilms' tumor gene, WT1, mRNA is down-regulated during induction of erythroid an  
 A:Reference number: I38504; PMID:94368704; PMID:8086342  
 A:Accession: I38504  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-18 <PHE>  
 A:Cross-references: EMBL:U06486; NID:9473563; PIDN:AAA62865.1; PID:9458432  
 R:Belletier, J.; Bruneau, W.; Kashan, C.E.; Maurer, S.M.; Mantvel, J.C.; Striegel, J.E.  
 Cell 67, 437-447, 1991  
 A:Title: Germ-line mutations in the Wilms' tumor suppressor gene are associated with abn  
 A:Reference number: I52811; PMID:92005721; PMID:1655284  
 A:Accession: I52811  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 355-365, 'H', 367-377 <PEL>  
 A:Cross-references: GB:S61513; NID:9237599; PIDN:AAZ0109.1; PID:9237600  
 A:Note: mutant form  
 R:Hamilton, T.B.; Barilla, K.C.; Romanuk, P.J.  
 Nucleic Acids Res. 23, 277-284, 1995  
 A:Title: High affinity binding sites for the Wilms' tumour suppressor protein WT1.  
 A:Reference number: I58315; PMID:95166649; PMID:7862533  
 A:Accession: I58315  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 'MGNNNNNNHSGHIEGRHM', 301-364, 'F', 366-386, 'T', 388-407, 411-449 <HAM>  
 A:Cross-references: GB:S75664; NID:9896246; PIDN:AA33443.1; PID:9896247  
 A:Note: this sequence is engineered  
 C:Genetics:

Qy 1 RMFPNAPYL 9  
 |||||  
 Db 126 RMFPNAPYL 134

RESULT 4

A:Gene: GDB:WT1  
 A:Cross-references: GDB:120496; OMIM:194070  
 A:Map position: 11p13-11p13  
 A:Insertions: 148/1, 189/1, 223/2, 249/2, 266/2, 298/3, 349/1, 379/1, 410/1  
 A:Note: mRNA transcripts containing both alternatively spliced regions are the most abundant  
 C:Keywords: alternative splicing; DNA binding; kidney; tumor suppressor; zinc finger  
 F:1-407/411-449/Product: Wilms tumor susceptibility protein WT1, splice form 1 #status predicted  
 F:1-249/267-449/Product: Wilms tumor susceptibility protein WT1, splice form 2 #status predicted  
 F:1-249/267-407/411-449/Product: Wilms tumor susceptibility protein WT1, splice form 3 #status predicted

A:Accession: A39692  
 C:Date: 30-Dec-1991 #sequence revision 30-Dec-1991 #text change 16-Feb-1997  
 A:Species: Mus musculus (house mouse)  
 A:Title: Isolation, characterization, and expression of the murine Wilms' tumor gene (WT)  
 A:Reference number: A39692; PMID:91141522; PMID:1671709  
 A:Accession: A39692  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-449 <BUC>  
 A:Cross-references: GB:M55512  
 C:Keywords: alternative splicing; DNA binding; transcription regulation; tumor suppressor

Query Match 100.0%; Score 51; DB 2; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 0.054; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
 |||||  
 Db 126 RMFPNAPYL 134

RESULT 5

A:Gene: GDB:WT1  
 A:Cross-references: GDB:120496; OMIM:194070  
 A:Map position: 11p13-11p13  
 A:Insertions: 148/1, 189/1, 223/2, 249/2, 266/2, 298/3, 349/1, 379/1, 410/1  
 A:Note: mRNA transcripts containing both alternatively spliced regions are the most abundant  
 C:Keywords: alternative splicing; DNA binding; kidney; tumor suppressor; zinc finger  
 F:1-407/411-449/Product: Wilms tumor susceptibility protein WT1, splice form 1 #status predicted  
 F:1-249/267-449/Product: Wilms tumor susceptibility protein WT1, splice form 2 #status predicted  
 F:1-249/267-407/411-449/Product: Wilms tumor susceptibility protein WT1, splice form 3 #status predicted

A:Accession: AD1343  
 C:Date: 27-Nov-2001 #sequence revision 27-Nov-2001 #text change 27-Nov-2001  
 A:Species: Listeria monocytogenes  
 A:Title: Comparative genomics of Listeria species.  
 A:Reference number: AB1077; PMID:21537279; PMID:11679669  
 A:Accession: AD1343  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-213 <GUA>  
 A:Cross-references: GB:NC\_003210; PIDN:CAD00226.1; PID:916411618; GSPDB:GN00177  
 A:Experimental source: strain EGD-e  
 C:Genetics:

Query Match 80.4%; Score 41; DB 2; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 FPNAPYL 9  
|||||  
Db 67 FPNAPYL 73

## RESULT 6

hypothetical protein homolog lin252 [imported] - *Listeria innocua* (strain C1p11262)  
C/Species: *Listeria innocua*  
C/Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C/Accession: AB1713  
R/Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fehli, H.; Jones, L.M.; Karet, U.  
Science 294, 849-852, 2001  
A/Authors: Kreft, J.; Kunz, M.; Kusch, F.; Kurpkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A./Title: Comparative genomics of *Listeria* species.  
A/Reference number: AB1077; MUID:21537279; PMID:11679669  
A/Accession: AB1713  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-213 <GLA>  
A/Cross-references: GB:AL592022; PIDN:CA937480.1; PID:gl6414764; GSPDB:GN00178  
A/Experimental source: strain C1p11262  
C/Genetics:  
A/Gene: lin252

Query Match 80.4%; Score 41; DB 2; Length 213;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 FPNAPYL 9  
|||||  
Db 67 FPNAPYL 73

## RESULT 7

hypothetical protein HI0177 - *Haemophilus influenzae* (strain Rd KW20)  
C/Species: *Haemophilus influenzae*  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 28-Jul-2000  
C/Accession: G64144  
R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Goeynne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.; Science 269, 496-512, 1995  
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A./Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.  
A/Reference number: A64000; MUID:95350630; PMID:7542800  
A/Accession: G64144  
A/Status: nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-262 <TIGR>  
A/Cross-references: GB:U32703; GB:142023; NID:g1573133; PIDN:AA021847.1; PID:g1573134; T  
A/Note: best homolog was a hypothetical protein from *Pseudomonas aeruginosa*  
C/Superfamily: conserved hypothetical protein HI0177

Query Match 78.4%; Score 40; DB 1; Length 262;  
Best Local Similarity 75.0%; Pred. No. 3.8;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 MFPNAPYL 8  
|||||  
Db 151 RVFNPSPY 158

## RESULT 8

C/Species: conserved hypothetical integral membrane protein TP0033 - *Syphilis spirochete*  
C/Species: *Treponema pallidum* subsp. *pallidum* (*Syphilis spirochete*)  
C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 05-Nov-1999  
C/Accession: C71375

R/Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin  
rean, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetzbach, T.; McDor  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998  
A/Title: Complete genome sequence of *Treponema pallidum*, the *Syphilis spirochete*.  
A/Reference number: A71250; MUID:98332770; PMID:9665876  
A/Accession: C71375

A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-203 <COL>  
A/Cross-references: GB:AE001188; GB:AE000520; NID:g3322282; PIDN:AA065028.1; PID:g3322288  
A/Experimental source: strain Nichols  
C/Genetics:  
A/Gene: TP0033

Query Match 76.5%; Score 39; DB 2; Length 203;  
Best Local Similarity 85.7%; Pred. No. 4.4;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 FPNAPYL 9  
|||||  
Db 63 FPNAPYL 69

## RESULT 9

probable hydrolase PA1202 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
C/Species: *Pseudomonas aeruginosa*  
C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C/Accession: F83495  
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
adman, S.; Van, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathog  
A/Reference number: A82950; MUID:20437337; PMID:10984043  
A/Accession: F83495  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-205 <STO>  
A/Cross-references: GB:AE004550; GB:AE004091; NID:g9947122; PIDN:AA04591.1; GSPDB:GN001;  
C/Genetics:  
A/Experimental source: strain PA01  
A/Gene: PA1202

Query Match 74.5%; Score 38; DB 2; Length 205;  
Best Local Similarity 75.0%; Pred. No. 7;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MFPNAPYL 9  
|||||  
Db 75 MFPQAPYL 82

## RESULT 10

AB2195  
serine esterase [imported] - *Nostoc* sp. (strain PCC 7120)  
C/Species: *Nostoc* sp. PCC 7120  
A/Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
C/Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C/Accession: AB2195  
R/Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matsumoto, A.; Iritani,  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*  
A/Reference number: AB1807; MUID:21595285; PMID:11759840  
A/Accession: AB2195  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-214 <KUR>  
A/Cross-references: GB:BA000019; PIDN:BA074812.1; PID:g17132207; GSPDB:GN00179  
A/Experimental source: strain PCC 7120  
C/Genetics:

A:Gene: all3113

Query Match 74.5%; Score 38; DB 2; Length 214;  
 Best Local Similarity 85.7%; Pred. No. 7.3;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 MFNPAPYL 8  
 DB 56 VFNPAPYL 62

## RESULT 11

E86408

F3H9.11 protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Nov-2001

C:Accession: E86408

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso, J.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizart, L.

Nature 408, 816-820, 2000

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, R.;

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: E86408

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-581 &lt;STO&gt;

A:Cross-references: GB:AE005172; NID:99795613; PIDN:PAF98431.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 74.5%; Score 38; DB 2; Length 581;  
 Best Local Similarity 87.5%; Pred. No. 22;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MFNPAPYL 8  
 DB 349 RMFPNARY 356

## RESULT 12

S42210

ISG-54K protein - Chinese hamster

C:Species: Cricetus griseus (Chinese hamster)

C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 07-May-1999

C:Accession: S42210

R:Bluyssen, H.R.; Vilestra, R.J.; van der Made, A.; Trapman, J.

Eur. J. Biochem. 220, 395-402, 1994

A:Title: The interferon-stimulated gene 54 K promoter contains two adjacent functional alpha inducibility.

A:Reference number: S42210; MUID:94170787; PMID:8125096

A:Accession: S42210

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-466 &lt;BLU&gt;

C:Superfamily: Interferon-induced 56K protein

Query Match 72.5%; Score 37; DB 2; Length 466;  
 Best Local Similarity 66.7%; Pred. No. 27;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 DB 201 RMSPNSPYV 209

## RESULT 13

S33558

unc-33 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 07-Apr-1994 #sequence\_revision 02-Jun-1994 #text\_change 21-Jul-2000

C:Accession: S33558; S33559; S24643; S24644

R:Li, W.; Herman, R.K.; Shaw, J.E.

Genetics 132, 675-689, 1992

A:Title: Analysis of the Caenorhabditis elegans axonal guidance and outgrowth gene unc-33

A:Reference number: S33558; MUID:93106371; PMID:1468626

A:Accession: S33558

A:Molecule type: DNA

A:Residues: 1-854 &lt;LIW1&gt;

A:Cross-references: EMBL:214148; NID:96899; PIDN:CAA78520.1; PID:96900

A:Accession: S33559

A:Molecule type: mRNA

A:Residues: 1-854 &lt;LIW2&gt;

A:Cross-references: EMBL:214146; NID:96903; PID:96904

C:Genetics:

A:Insertions: 14/2; 68/1; 129/3; 151/3; 182/1; 255/3; 361/2; 660/1; 790/3

C:Keywords: alternative initiator

F:1-854/Product: unc-33 protein (long form) #status predicted &lt;MAT1&gt;

F:176-854/Product: unc-33 protein (intermediate form) #status predicted &lt;MAT2&gt;

F:332-854/Product: unc-33 protein (short form) #status predicted &lt;MAT3&gt;

OY 1 MFNPAPYL 9  
 DB 773 RLSPNSPYL 781

## RESULT 14

A55478

neuronal apoptosis inhibitory protein - human

N:Alternate names: NAIP

C:Species: Homo sapiens (man)

C:Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 02-Feb-2001

C:Accession: A55478

R:Roy, N.; Mahadevan, M.S.; McLean, M.; Shuttler, G.; Yarghi, Z.; Farahani, R.; Baird, S

Cell 80, 167-178, 1995

A:Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in indi

A:Reference number: A55478; MUID:95112344; PMID:7813013

A:Accession: A55478

A:Molecule type: mRNA

A:Residues: 1-1232 &lt;ROY&gt;

A:Cross-references: GB:U19251

C:Genetics:

A:Gene: GDB:SMA@; SMA

A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300

A:Map position: Sg12.2-Sg13

C:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane prote

F:94-110/Domain: transmembrane #status predicted &lt;TM1&gt;

F:470-477/Region: nucleotide-binding motif A (P-loop)

F:478-496/Domain: transmembrane #status predicted &lt;TM2&gt;

F:476/Binding site: ATP (Lys) #status predicted

F:618,632,923,923,1035/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 72.5%; Score 37; DB 2; Length 1232;  
 Best Local Similarity 66.7%; Pred. No. 79;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MFNPAPYL 9  
 DB 337 RCFNCPFL 345

## RESULT 15

S17463

glutathione transferase (EC 2.5.1.18) class mu chain yb5 - mouse (Fragments)

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 16-Feb-1997



C;Accession: S17463  
R;Hayes, J.D.; Kerr, L.A.; Peacock, S.D.; Cronshaw, A.D.; Mclellan, L.I.  
Biochem. U. 277, 501-512; 1991  
A;Title: Hepatic glutathione S-transferases in mice fed on a diet containing the anticarcinogenic elution of the glutathione-Sepharose affinity matrix.  
A;Reference number: S16933; MUID:91315425; PMID:1859377  
A;Accession: S17463  
A;Molecule type: protein  
A;Residues: 1-38;39-64;65-85 <HAY>  
C;Superfamily: glutathione transferase  
C;Keywords: blocked amino end; dimer; transferase

Query March 70.6%; Score 36; DB 2; Length 85;  
Best Local Similarity 85.7%; Pred. No. 6.3;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FPNAPYL 9  
|||  
Db 23 FPNLPYL 29

Search completed: January 21, 2004, 08:44:43  
Job time : 22 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 21, 2004, 08:36:24 ; Search time 11 Seconds  
(without alignments)  
38.476 Million cell updates/sec

Title: US-09-625-963A-1  
Sequence: 1 RMPNPAPYL 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	448	1	WT1_RAT
2	51	100.0	449	1	P4952_rattus norv
3	51	100.0	449	1	P19544 homo sapien
4	51	100.0	449	1	WT1_MOUSE
5	40	78.4	262	1	WT1_PIG
6	37	72.5	468	1	YPTO_HAERIN
7	37	72.5	854	1	IF22_CRILLO
8	37	72.5	1403	1	UN33_CABEL
9	36	70.6	217	1	Q13075 homo sapien
10	36	70.6	217	1	BTM1_HUMAN
11	36	70.6	217	1	BTM1_MOUSE
12	36	70.6	217	1	BTM1_MOUSE
13	36	70.6	217	1	BTM1_MOUSE
14	36	70.6	217	1	BTM1_MOUSE
15	36	70.6	217	1	BTM1_MOUSE
16	36	70.6	217	1	BTM1_MOUSE
17	36	70.6	217	1	BTM1_MOUSE
18	36	70.6	217	1	BTM1_MOUSE
19	36	70.6	217	1	BTM1_MOUSE
20	36	70.6	217	1	BTM1_MOUSE
21	36	70.6	217	1	BTM1_MOUSE
22	36	70.6	218	1	BTM1_MOUSE
23	36	70.6	218	1	BTM1_MOUSE
24	36	70.6	219	1	BTM1_MOUSE
25	36	70.6	224	1	BTM1_MOUSE
26	36	70.6	224	1	BTM1_MOUSE
27	36	70.6	225	1	BTM1_MOUSE
28	36	70.6	358	1	BTM1_MOUSE
29	36	70.6	370	1	BTM1_MOUSE
30	36	70.6	370	1	BTM1_MOUSE
31	36	70.6	381	1	BTM1_MOUSE
32	36	70.6	382	1	BTM1_MOUSE
33	36	70.6	382	1	BTM1_MOUSE

34	36	70.6	487	1	C8B1_ESCCA	064899 eschecholz
35	36	70.6	488	1	C8B2_ESCCA	064900 eschecholz
36	36	70.6	509	1	C4A1_DROME	09vms9 drosophila
37	36	70.6	618	1	BIR2_HUMAN	Q13490 homo sapien
38	35	68.6	273	1	TRY6_ANOGA	P35040 anopheles g
39	35	68.6	380	1	TPSA_CABEL	077081 caenorhabdi
40	35	68.6	500	1	C81F_ARATH	065790 arabidopsis
41	34	66.7	180	1	YH95_AQUAE	067664 aquifex aeo
42	34	66.7	260	1	YH20_PASMU	09ckas pasteurella
43	34	66.7	855	1	ST14_MOUSE	P56677 mus musculu
44	34	66.7	1097	1	CCT_DROME	096433 drosophila
45	33	64.7	110	1	YA61_STRMU	P96468 streptococc

## ALIGNMENTS

RESULT 1  
WT1\_RAT  
ID WT1\_RAT STANDARD; PRT; 448 AA.  
AC P4952;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Wt1s, tumor protein homolog.  
DE Wt1 OR Wt-1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_Taxid=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).  
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;  
RX MEDLINE=93046155; PubMed=1330293;  
RA Sharma P.M., Yang X., Bowman M., Roberts V., Sukumar S.;  
RT "Molecular cloning of rat Wt1s, tumor complementary DNA and a study  
of messenger RNA expression in the urogenital system and the brain.";  
RL Cancer Res. 52:6407-6412(1992).  
CC -1- FUNCTION: POTENTIAL ROLE IN TRANSCRIPTIONAL REGULATION. RECOGNIZES  
AND BINDS TO THE DNA SEQUENCE 5'-GGCCCCGGC-3'.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named Isoforms=4;  
CC Name=1;  
CC IsoId=P4952-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=P4952-2; Sequence=VSP\_006872, VSP\_006873;  
CC Name=3;  
CC IsoId=P4952-3; Sequence=VSP\_006872;  
CC Name=4;  
CC IsoId=P4952-4; Sequence=VSP\_006873;  
CC -1- TISSUE SPECIFICITY: Kidney.  
CC -1- DEVELOPMENTAL STAGE: Expressed during kidney development.  
CC -1- SIMILARITY: BELONGS TO THE EGR FAMILY OF C2H2-TYPE ZINC-FINGER  
PROTEINS.  
CC -1- SIMILARITY: Contains 4 C2H2-type zinc fingers.  
CC -----  
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CC -----  
CC EMBL: X69716; CAA49373.1; --  
CC HSSP: P08046; 1AAY.  
CC TRANSFAC: T02352;  
CC InterPro: IPR000976; Wt1s tumour.  
CC InterPro: IPR007087; Znf\_C2H2.  
CC Pfam: PF02165; WT1; 1.  
CC Pfam: PF00096; Zf-C2H2; 4.  
CC PRINTS: PR00049; Wt1sTUMOUR.



RT Cell 67:437-447(1991).  
 RN [13]  
 RP VARIANTS DDS.  
 RX MEDLINE=93265053; PubMed=1338906;  
 RA Baird P.N., Santos A., Groves N., Jadesic L., Cowell J.K.;  
 RT "Constitutional mutations in the WT1 gene in patients with  
 RT Denys-Drash syndrome.";  
 RL Hum. Mol. Genet. 1:301-305(1992).  
 RN [14]  
 RP SEQUENCE OF 385-405 FROM N.A., AND VARIANT DDS TRP-394.  
 RX MEDLINE=93250986; PubMed=1302008;  
 RA Bruening W., Bardeesy N., Silverman B.L., Cohn R.A., Machin G.A.,  
 RA Aronson A.J., Housman D., Pelletier J.;  
 RT "Germline intronic and exonic mutations in the Wilms' tumour gene  
 RT (WT1) affecting urogenital development.";  
 RL Nat. Genet. 1:144-148(1992).  
 RN [15]  
 RP VARIANTS DDS.  
 RX MEDLINE=93271983; PubMed=8388765;  
 RA Little M.H., Williamson K.A., Mannens M., Kelsey A., Goeden C.,  
 RA Haseltine N.D., van Heyningen V.;  
 RT "Evidence that WT1 mutations in Denys-Drash syndrome patients may act  
 RT in a dominant-negative fashion.";  
 RL Hum. Mol. Genet. 2:259-264(1993).  
 RN [16]  
 RP VARIANTS DDS TRP-394 AND PRO-398.  
 RX MEDLINE=94125627; PubMed=8295405;  
 RA Teuda M., Sakiyama T., Kitagawa T., Watanabe S., Watanabe T.,  
 RA Takahashi S., Kawaguchi H., Ito K.;  
 RT "Molecular analysis of two Japanese cases of Denys-Drash syndrome.";  
 RL J. Inher. Metab. Dis. 16:876-880(1993).  
 RN [17]  
 RP VARIANTS MESOTHELIOMA GUY-273.  
 RX MEDLINE=94004972; PubMed=8401592;  
 RA Park S., Schalling M., Bernard A., Maheswaran S., Shipley G.C.,  
 RA Roberts D., Fletcher J., Shipman R., Rheinwald J., Demetri G.,  
 RA Griffin J., Minden M., Housman D.E., Haber D.A.;  
 RT "The Wilms tumour gene WT1 is expressed in murine mesoderm-derived  
 RT tissues and mutated in a human mesothelioma.";  
 RL Nat. Genet. 4:415-420(1993).  
 RN [18]  
 RP VARIANTS DDS ARG-377.  
 RX MEDLINE=94156335; PubMed=8112732;  
 RA Nordenskjold A., Friedman E., Anyret M.;  
 RT "WT1 mutations in patients with Denys-Drash syndrome: a novel mutation  
 RT in exon 8 and paternal allele origin.";  
 RL Hum. Genet. 93:115-120(1994).  
 RN [19]  
 RP VARIANTS DDS TYR-373.  
 RX MEDLINE=97114281; PubMed=8956030;  
 RA Ghahremani M., Chan C.B., Bistritz T., Aladjem M.M., Tiedler M.,  
 RA Pelletier J.;  
 RT "A novel mutation H373Y in the Wilms' tumor suppressor gene, WT1,  
 RT associated with Denys-Drash syndrome.";  
 RL Hum. Hered. 46:336-338(1996).  
 RN [20]  
 RP VARIANTS WT SER-181 AND ALA-253.  
 RX MEDLINE=97266681; PubMed=9108089;  
 RA Schumacher V., Schneider S., Fige A., Wildhardt G., Harms D.,  
 RA Schmidt D., Weich A., Ludwig R., Royer-Pokora B.;  
 RT "Correlation of germ-line mutations and two-hit inactivation of the  
 RT WT1 gene with Wilms tumors of stromal-predominant histology.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3972-3977(1997).  
 RN [21]  
 RP VARIANTS IDMS TYR-377, LEU-383 AND ASN-396, VARIANTS DDS CYS-366;  
 RP GUN-394, TRP-394 AND PRO-398, AND VARIANT WT ASN-223.  
 RX MEDLINE=98198341; PubMed=9529364;  
 RA Ceccipierre C., Denamur E., Henry I., Cabanis M.-O., Luce S.,  
 RA Cecille A., Elion J., Peuchmair M., Lotrat C., Naudet P.,  
 RA Gubler M.-C., Junien C.;  
 RT "Identification of constitutional WT1 mutations, in patients with  
 RT isolated diffuse mesangial sclerosis, and analysis of  
 RT genotype/phenotype correlations by use of a computerized mutation

RT database.";  
 RL Am. J. Hum. Genet. 62:824-833(1998).  
 RN [22]  
 RP VARIANTS DDS TYR-355, HIS-366 AND ARG-385.  
 RX MEDLINE=9815435; PubMed=9475094;  
 RA Kikuchi H., Takata A., Akasaka Y., Fukuzawa R., Yoneyama H.,  
 RA Kurosawa Y., Honda M., Kamiyama Y., Hata J.;  
 RT "Do intronic mutations affecting splicing of WT1 exon 9 cause Fraiser  
 RT syndrome?"  
 QY 1 RMEPNAPYL 9  
 Db 126 RMEPNAPYL 134  
 Query Match 100.0%; Score 51; DB 1; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 0.031;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 3  
 WT1\_MOUSE STANDARD; PRT; 449 AA.  
 ID WT1\_MOUSE  
 AC P22561;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Wilms' tumor protein homolog.  
 GN WT1 OR WT-1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1, 2, 3 AND 4).  
 RX MEDLINE=9141522; PubMed=1671709;  
 RA Buckler A.J., Pelletier J., Haber D.A., Glaser T., Housman D.E.;  
 RT "Isolation, characterization, and expression of the murine Wilms'  
 RT tumor gene (WT1) during kidney development.";  
 RL Mol. Cell. Biol. 11:1707-1712(1991).  
 CC -1- FUNCTION: POTENTIAL ROLE IN TRANSCRIPTIONAL REGULATION. RECOGNIZES  
 CC AND BINDS TO THE DNA SEQUENCE 5'-CGCCCCCG-3'.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1;  
 CC IsoId=P22561-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=P22561-2; Sequence=VSP\_006868, VSP\_006869;  
 CC Name=3;  
 CC IsoId=P22561-3; Sequence=VSP\_006868;  
 CC Name=4;  
 CC IsoId=P22561-4; Sequence=VSP\_006869;  
 CC -1- TISSUE SPECIFICITY: Kidney.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING KIDNEY DEVELOPMENT.  
 CC -1- SIMILARITY: BELONGS TO THE EGR FAMILY OF C2H2-TYPE ZINC-FINGER  
 CC PROTEINS.  
 CC -1- SIMILARITY: Contains 4 C2H2-type zinc fingers.  
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 CC -----  
 CC EMBL: M55512; AAA0573.1; -.  
 CC HSPB: P08046; 1AAY.  
 CC TRNSPAC: T02351; -.  
 CC MGP: MGI.98968; WLI.  
 CC GO: GO:0005634; C:nucleus; IDA.  
 CC GO: GO:0005515; F:protein binding activity; IPI.  
 CC GO: GO:0001554; P:eye morphogenesis; IMP.

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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; AB081969; BAA28147.1; .
DR	HSSP; P08046; IAAV.
DR	InterPro; IPRO00976; Wlms tumour.
DR	InterPro; IPRO07087; Znf_C2H2.
DR	Pfam; PF02165; WT1; 1.
DR	Pfam; PF00096; zf-C2H2; 4.
DR	PRINTS; PRO0049; WIMSTUMOUR.
DR	Prodrom; PD000003; Znf_C2H2; 2.
DR	SMART; SMO0355; Znf_C2H2; 4.
DR	PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR	PROSITE; PS01017; ZINC_FINGER_C2H2_2; 4.
KW	Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;
KW	Transcription regulation; Alternative splicing; Anti-oncogene.
FT	DOMAIN 28 83
FT	ZN_FING 323 347
FT	ZN_FING 353 377
FT	ZN_FING 383 405
FT	ZN_FING 414 438
FT	VARSPLIC 249 265
FT	Mising (in isoform 2 and isoform 3).
FT	/Frtid=VSP_006870.
FT	Missing (in isoform 2 and isoform 4).
FT	/Frtid=VSP_006871.
SO	SEQUENCE 449 AA; 4916 MW; 9C3B557B56FA7A753 CRC64;
Oy	Query Match 100.0%; Score 51; DB 1; Length 449;
Db	Best Local Similarity 100.0%; Pred. No. 0.031;
	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	1 RMPNPAPYL 9
	126 RMPNPAPYL 134
RESULT 5	
ID	YFIO_HAEIN STANDARD; PRT; 262 AA.
AC	P44553;
DT	01-NOV-1995 (Rel. 32, Created)
DT	01-NOV-1995 (Rel. 32, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Purative lipoprotein HI0177 precursor.
GN	HI0177.
OS	Haemophilus influenzae.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC	Pasteurellaceae; Haemophilus.
OX	NCBI_TaxID=727;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Rd / KW20 / ATCC 51907;
RX	MEDLINE=95350630; PubMed=7542800;
RA	Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA	Keilavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA	McMenemy K., Sutton G., Fitzhugh B., Fields C.A., Gocayne J.D.,
RA	Scott J.D., Shiley R., Iju L.-I., Glodek A., Kelley J.M.,
RA	Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA	Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.W., Brandon R.C.,
RA	Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA	Venter J.C.;
RT	"Whole-genome random sequencing and assembly of Haemophilus influenzae
RT	Rd.";
RL	Science 269:496-512(1995).
RN	[2]
RP	IDENTIFICATION BY MASS SPECTROMETRY.

```

RX MEDLINE=20137488; PubMed=10675023;
RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
RA Gray C., Fountoulakis M.;
RT "Two-dimensional map of the proteome of Haemophilus influenzae."
RL Electrophoresis 21:411-429(2000).
CC
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (By similarity).
CC
CC -1- SIMILARITY: BELONGS TO THE UPF0169 (COM1) FAMILY.
CC
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CC
CC -----
DR EMBL: U32703; AAC21447.1; -.
DR PIR: G64144; G64144.
DR TIGR: H10177; -.
DR InterPro: IPR005156; UPF0169.
DR Pfam: PF03696; UPF0169; 1.
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW Membrane; Lipoprotein; Signal; Complete proteome.
FT SIGNAL 1 18
FT CHAIN 19 262
FT LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 262 AA; 29347 MW; 1DD9FFFE568D2B7B CRC64;

Query March 78.4%; Score 40; DB 1; Length 262;
Beet Local Similarity 75.0%; Pred. No. 2;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMPFNAPY 8
Db 151 RVFNPSPY 158
|:|:|:|
|:|:|:|

RESULT 6
IFT2_CRILLO
ID IFT2_CRILLO STANDARD; PRT; 468 AA.
AC Q60462;
NC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interferon-induced protein with tetratricopeptide repeats 2 (IFT2-2)
DE (Interferon-induced 54 kDa protein) (IFI-54K) (CL-54 K).
GN IFT2 OR IFI54.
OS Citicellus longicaudatus (long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OC NCBI_TaxID=10030;
CX [1]
SV SEQUENCE FROM N.A.
RX MEDLINE=94170787; PubMed=8125096;
RA Bluyssen J.A.R., Vlietstra R.J., Van der Made A., Trapman J.;
RT "The interferon-stimulated gene 54 k promoter contains two adjacent
RT functional interferon-stimulated response elements of different
RT strength, which act synergistically for maximal interferon-alpha
RT inducibility."
RT Eur. J. Biochem. 220:395-402(1994).
CC -1- INDUCTION: By interferons.
CC -1- SIMILARITY: BELONGS TO THE IFT2 FAMILY.
CC -1- SIMILARITY: Contains 6 TPR repeats.
CC
CC -----
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CC      EMBL; X77259; CA54477.1; -.
DR      InterPro; IPR001440; TPR.
DR      Pfam; PF00515; TPR; 4.
KW      Repeat; TPR repeat; Interferon induction.
FT      REPEAT          94      127      TPR 1.
FT      REPEAT          138      171      TPR 2.
FT      REPEAT          175      208      TPR 3.
FT      REPEAT          242      275      TPR 4.
FT      REPEAT          327      360      TPR 5.
FT      REPEAT          364      398      TPR 6.
SQ      SEQUENCE        468 AA;  55045 MM;  90928878P81B1E27 CRC64;

Query Match      72.5%; Score 37; DB 1; Length 468;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1  RMPNAPYL 9
DB      203  RMSPSPTV 211

RESULT 7
UN33  CABEL
ID      UN33  CABEL      STANDARD;      PRT;      854 AA.
AC      001630;
DT      01-JUL-1993 (Rel. 26, Created)
DT      01-JUL-1993 (Rel. 26, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Uncoordinated protein 33 (Protein unc-33).
DN      UNC-33 OR Y37E11C.1.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Rhabditidae;
OC      Rhabditidae; Pelodierinae; Caenorhabditis.
OX      NCB1_TaxID=6239;
RN      [1]
RP      SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING.
RC      STRAIN=Bristol N2; TISSUE=embryo;
RX      MEDLINE=93106371; PubMed=1468626;
RA      Li W., Herman R.K., Shaw J.E.;
RT      "Analysis of the Caenorhabditis elegans axonal guidance and outgrowth
RL      gene unc-33."
RL      Genetics 132:675-689(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Bristol N2;
RA      Wilson R., Maggi L., Waterston B.;
RL      Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      REVISIONS, AND ALTERNATIVE SPLICING.
RL      Waterston R.;
RL      Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: INVOLVED IN AXONAL GUIDANCE AND OUTGROWTH.
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=3;
CC      Name=1; Synonyms=a;
CC      IsoId=Q01630-1; Sequence=Displayed;
CC      Name=i1; Synonyms=b, 72.1 kDa;
CC      IsoId=Q01630-2; Sequence=VSP_001310;
CC      Name=i1i1; Synonyms=c, 55.5 kDa;
CC      IsoId=Q01630-3; Sequence=VSP_001311;
CC      -1- TISSUE SPECIFICITY: Expressed exclusively within neuronal
CC      processes after early embryogenesis.
CC      -1- SIMILARITY: BELONGS TO THE DEHYDROPRIMIDINASE FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).

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Query Match	Best Local Similarity	Matches	Score	DB 1	Length	854	
		6; Conservative	66.7%;				
Qy	1 RMFPNAPYL 9						
	:						
Db	773 RLSPNSPYL 781						
RESULT 8							
B1R1_HUMAN	STANDARD;	PRT;	1403 AA.				
AC	Q13075; Q75857; Q13730; Q99786;						
DT	01-NOV-1997 (Rel. 35, Created)						
DT	16-OCT-2001 (Rel. 40, Last sequence update)						
DT	28-FEB-2003 (Rel. 41, Last annotation update)						
DE	Basal/ovital IAP repeat-containing protein 1 (Neuronal apoptosis inhibitory protein).						
DE	B1R1 OR NAIIP						
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
OX	NCBI_TaxID=9606;						
OX	[1]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=Petal brain;						
RC	MEDLINE=95112344; PubMed=7813013;						
RA	Roy N., Mahadevan M.S., McLean W., Shuttler G., Yarghi Z.,						
RA	Farahini R., Baird S., Besner-Johnston A., Lefebvre C., Kang X.,						
RA	Saikh M., Aubry H., Tamai K., Guan X., Iannou P., Crawford T.O.,						
RA	de Jong P.J., Suh L., Ikeda J., Korneluk R.G., Mackenzie A.J.						
RT	"The gene for neuronal apoptosis inhibitory protein is partially						
RT	deleted in individuals with spinal muscular atrophy."						
RL	Cell 80:167-178 (1995).						
RL	[2]						
RP	SEQUENCE FROM N.A., AND REVISIONS.						
RC	TISSUE=Brain;						
RC	MEDLINE=98163755; PubMed=9503025;						
RA	Chen Q., Baird S.D., Mahadevan M., Besner-Johnston A., Farahani R.,						
RA	Xu X.-Y., Kang X., Lefebvre C., Ikeda J.-E., Korneluk R.G.,						
RA	Mackenzie A.E.;						
RT	"Sequence of a 131-kb region of 5q13.1 containing the spinal muscular						
RT	atrophy candidate genes SMN and NAIIP."						
RL	Genomics 48:121-127 (1996).						
RL	[3]						
RP	SEQUENCE OF 386-623 FROM N.A.						
RA	der Steeger G., Draaijers T.G., Grootscholten P.M., Olinga J.,						
RA	Anzavino R., Velona I., Brane C., Scheffer H., van Ommen G.J.B.,						

Query Match	Best Local Similarity	Score 37;	DB 1;	Length 1403;
RA Buys C.H.C.M.?				
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.				
RN [4]				
RP SEQUENCE OF 222-1403 FROM N.A.				
RA Jones K., Graves T., McPherson J.;				
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.				
RN [5]				
RP FUNCTION.				
RC TISSUE=Liver;				
EX MEDLINE=96149249; Pubmed=8552191;				
RA Liston P., Roy N., Tamai K., Lefebvre C., Baid S., Chetnon-Horvat G.,				
RA Farahant R., Mclean M., Ikeda Y., Mackenzie A., Korneluk R.G.;				
RT "Suppression of apoptosis in mammalian cells by NAIP and a related				
RL family of IAP genes.";				
Nature 379:349-353(1996).				
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF				
CC SIGNALS.				
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY				
CC NEURONS. FOUND IN LIVER AND PLACENTA, AND IN A LESSER EXTENT IN				
CC SPINAL CORD.				
CC -1- DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN				
CC INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMA TYPE 1). SMAS				
CC ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE I				
CC (MERDING-HOFFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE				
CC II (MOHLFART-KUGELBERG-MELANDER DISEASE) BASED UPON THE AGE OF				
CC ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE				
CC CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO				
CC PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000				
CC NEWBORNS.				
CC -1- SIMILARITY: Contains 3 BIR repeats.				
CC -1- SIMILARITY: Contains 1 NACHT domain.				
CC -----				
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CC or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC -----				
CC EMBL; U19251; AAC52045.1; -;				
DR EMBL; U80017; AAC52047.1; -;				
DR EMBL; U21913; AAA64504.1; -;				
DR EMBL; AC005031; AAC62261.1; -;				
DR HSSP; Q13490; IQH.				
DR Genew; HGNC:7634; BIRC1.				
DR MIM; 600355; -;				
DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.				
DR GO; GO:0006916; P:anti-apoptosis; TAS.				
DR GO; GO:0007359; P:neurogenesis; TAS.				
DR InterPro; IPR003593; AAA_ATPase.				
DR InterPro; IPR007111; NACHT_NTPase.				
DR Pfam; PF00653; BIR; 3.				
DR SMART; SM00382; AAA; 1.				
DR SMART; SM00238; BIR; 3.				
DR PROSITE; PS01282; BIR_REPEAT_1; 3.				
DR PROSITE; PS0143; BIR_REPEAT_2; 3.				
DR PROSITE; PS0837; NACHT; 1.				
KW Apoptosis; Repeat.				
FT REPEAT 60 127 BIR 1.				
FT REPEAT 159 227 BIR 2.				
FT REPEAT 278 345 BIR 3.				
FT DOMAIN 464 758 NACHT.				
FT CONFLICT 222 223 PK -> YR (IN REF. 4).				
FT CONFLICT 386 387 VP -> ST (IN REF. 3).				
FT CONFLICT 535 535 M -> V (IN REF. 3).				
FT CONFLICT 553 553 Y -> H (IN REF. 3).				
FT CONFLICT 1228 1231 MISSING (IN REF. 4).				
SQ SEQUENCE 1403 AA; 159613 MW; 566304C154DASE64 CRC64;				



Matches	6;	Conservative	1;	Mismatches	2;	Indels	0;	Gaps	0
Qy		1 RMEFNAPYL 9							
Db		337 RCFPNCPEL 345							
RESULT 9									
GTW1	HUMAN	STANDARD;	PRT;	217	AA.				
ID	GTW1_HUMAN								
AC	P09488;								
DT	01-MAR-1989 (Rel. 10, Created)								
DT	01-FEB-1991 (Rel. 17, Last sequence update)								
DT	28-FEB-2003 (Rel. 41, Last annotation update)								
DE	Glutathione S-transferase Mu 1 (EC 2.5.1.18) (GSTM1-1) (HB subunit 4)								
DE	(GSTM1) (GSTM1a-1a) (GSTM1b-1b) (GST class-mu 1).								
GN	GTW1 OR GST1.								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=88335606; PubMed=3419925;								
RA	DeJong J.L., Chang C.M., Whang Peng J., Knutsen T., Tu C.-P.D.;								
RT	"The human liver glutathione S-transferase gene superfamily:								
RT	expression and chromosome mapping of an Hb subunit cDNA.";								
RL	Nucleic Acids Res. 16:8541-8554(1988).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=89017184; PubMed=3174634;								
RA	Seidegard J., Vorachek W.R., Pero R.W., Pearson W.R.;								
RT	"Hereditary differences in the expression of the human glutathione								
RT	transferase active on trans-stilbene oxide are due to a gene								
RT	deletion.";								
RL	Proc. Natl. Acad. Sci. U.S.A. 85:7293-7297(1988).								
RN	[3]								
RP	SEQUENCE OF 1-188 FROM N.A.								
RX	MEDLINE=93228631; PubMed=8471052;								
RA	Zhong S., Spurr N.K., Hayes J.D., Wolf C.R.;								
RT	"Deduced amino acid sequence, gene structure and chromosomal location								
RT	of a novel human class Mu glutathione S-transferase, GSTM4.";								
RL	Biochem. J. 291:41-50(1993).								
RN	[4]								
RP	SEQUENCE OF 59-117 FROM N.A.								
RX	MEDLINE=90301515; PubMed=2362832;								
RA	Comstock K.E., Sanderson B.J.S., Claflin G., Henner W.D.;								
RT	"GST1 gene deletion determined by polymerase chain reaction.";								
RL	Nucleic Acids Res. 18:3670-3670(1990).								
RN	[5]								
RP	SEQUENCE OF 1-23.								
RX	MEDLINE=86042634; PubMed=3864155;								
RA	Mannervik B., Alin P., Guttenberg C., Jenson H., Tahir M.K.,								
RA	Warhol M., Joernvall H.;								
RT	"Identification of three classes of cytosolic glutathione transferase								
RT	common to several mammalian species: correlation between structural								
RT	data and enzymatic properties.";								
RL	Proc. Natl. Acad. Sci. U.S.A. 82:7202-7206(1985).								
RN	[6]								
RP	SEQUENCE OF 1-23.								
RX	MEDLINE=85154554; PubMed=3979555;								
RA	Alin P., Mannervik B., Joernvall H.;								
RT	"Structural evidence for three different types of glutathione								
RT	transferase in human tissues.";								
RL	FEBS Lett. 182:319-322(1985).								
RN	[7]								
RP	SEQUENCE OF 52-59, AND MASS SPECTROMETRY.								
RC	TISSUE=Liver;								
RX	MEDLINE=21088920; PubMed=11271497;								
RA	Hubbard M.J., McHugh N.J.;								

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RN [8] CRYSTALLOGRAPHY (2.68 ANGSTROMS), AND MUTAGENESIS OF HIS-107.
RP MEDLINE=99130249; PubMed=9930979.
RX Patcokovsky Y.V., Patcokovska L.N., Listowsky I.;
RA "Functions of Hs107 in the catalytic mechanism of human glutathione
RT S-transferase hGSTM1a."
RL Biochemistry 38:1193-1202(1999).
CC -1- FUNCTION: CONUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER
CC OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.
CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: THIS IS A LIVER ISOZYME.
CC -1- POLYMORPHISM: THERE ARE TWO ALLELES, GSTM1A AND GSTM1B WHICH
CC DIFFER IN POSITION 172.
CC -1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. MU FAMILY.
CC -----
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CC -----
DR EMBL; X08020; CAA30821.1; -.
DR EMBL; J03817; AAA59203.1; -.
DR EMBL; X68676; CAA48636.1; -.
DR EMBL; X51451; CAA35817.1; -.
DR PIR; S01719; S01719.
DR PDB; 1GTU; 02-FEB-99.
DR Genem; HGNC:4632; GSTM1.
DR MIM; 138350; -.
DR GO; GO:0004364; F:glutathione transferase activity; TAS.
DR GO; GO:0008181; F:tumor suppressor; TAS.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR003081; GST_mu.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
DR PRINTS; PRO1267; GSTRNSFRASEM.
DR Transferase; Multigene family; Polymorphism; 3D-structure.
KM INIT MET 0
FT FT 172 172
FT VARIANT
FT 209 209
FT MUTAGEN 107 107
FT CONFLICT 43 43
FT STRAND 2 7
FT HELIX 11 13
FT HELIX 14 22
FT TURN 23 24
FT STRAND 27 32
FT HELIX 43 49
FT TURN 50 50
FT STRAND 61 64
FT TURN 65 66
FT STRAND 67 70
FT HELIX 72 82
FT TURN 83 84
FT HELIX 90 115
FT TURN 117 118
FT HELIX 119 141
FT TURN 142 143
FT STRAND 146 146
FT TURN 147 148
FT STRAND 149 149
FT HELIX 154 169
FT TURN 171 176
FT HELIX 178 188
FT TURN 189 189

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FT HELIX 191 197
FT TURN 198 198
FT TURN 210 211
SQ SEQUENCE 217 AA; 25580 MW; ABBB0713BA75EAB CRC64;
Query Match 70.6%; Score 36; DB 1; Length 217;
Best Local Similarity 85.7%; Pred. No. 9.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 PPNAPYL 9
Db 56 PPNAPYL 62
RESULT 10
GTML MOUSE STANDARD; PRT; 217 AA.
ID GTML MOUSE
AC P10649;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Glutathione S-transferase Mu 1 (EC 2.5.1.18) (GST class-mu 1)
DE (Glutathione S-transferase GST-7) (pMG110) (GST 1-1).
GN GSTM1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88330838; PubMed=3417659;
RA Pearson W.R., Reinhardt J., Sisk S.C., Anderson K.S., Adler P.N.;
RT "Tissue-specific induction of murine glutathione transferase mRNAs by
RT butylated hydroxyanisole."
RL J. Biol. Chem. 263:13324-13332(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90094327; PubMed=2689439;
RA Townsend A.J., Goldsmith M.E., Pickett C.B., Cowan K.H.;
RT "Isolation, characterization, and expression in Escherichia coli of
RT two murine Mu class glutathione S-transferase cDNAs homologous to the
RT rat subunits 3 (Yb1) and 4 (Yb2)."
RL J. Biol. Chem. 264:21582-21590(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93290350; PubMed=8512323;
RA Reinhardt J., Pearson W.R.;
RT "The structure of two murine class-mu glutathione transferase genes
RT coordinately induced by butylated hydroxyanisole."
RL Arch. Biochem. Biophys. 303:383-393(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Martins K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelman M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cantini P., Prange C.J.,
RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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RN [5]
RP PRELIMINARY SEQUENCE OF 1-40.
RX MEDLINE=83109018; PubMed=6822548;
RA Pearson W.R., Windle J.J., Morrow J.F., Benson A.M., Talalay P.;
RT "Increased synthesis of glutathione S-transferases in response to
RT anticarcinogenic antioxidants. Cloning and measurement of messenger
RT RNA."
RL J. Biol. Chem. 258:2052-2062(1983).
RN [6]
RP PRELIMINARY SEQUENCE OF 1-24.
RX MEDLINE=86042634; PubMed=3864155;
RA Mannervik B., Alin P., Guthenberg C., Jansson H., Tahir M.K.,
RA Warholm M., Joernvall H.;
RT "Identification of three classes of cytosolic glutathione transferase
RT common to several mammalian species: correlation between structural
RT data and enzymatic properties."
RL Proc. Natl. Acad. Sci. U.S.A. 82:7202-7206(1985).
RN [7]
RP CHARACTERIZATION.
RC STRAIN=CD-1; TISSUE=Liver;
RX MEDLINE=96189427; PubMed=8605288;
RA Mitchell A.E., Morin D., Lame M.W., Jones A.D.;
RT "Purification, mass spectrometric characterization, and covalent
RT modification of murine glutathione S-transferases."
RL Chem. Res. Toxicol. 8:1054-1062(1995).
CC -1- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER
CC OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.
CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MASS SPECTROMETRY: MW=25838.4; MW ERR=2; METHOD=Electrospray.
CC -1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. MU FAMILY.
CC -----
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CC -----
DR EMBL: J03952; AAA37747.1; -.
DR EMBL: J04632; AAA37705.1; -.
DR EMBL: L13448; -. NOT ANNOTATED_CDS.
DR EMBL: BC003822; AA03822.1; -.
DR PIR: S33860; S33860.
DR HSSP: P04905; 2GST.
DR SWISS-2DPAGE: P10649; MOUSE.
DR MGD: MGI:95860; Gstm1.
DR InterPro: IPR004046; GST_Cterm.
DR InterPro: IPR003081; GST_mu.
DR InterPro: IPR004045; GST_Nterm.
DR Pfam: PF00043; GST_C_1.
DR Pfam: PF02798; GST_N_1.
DR PRINTS: PR01267; GSTRNSFRASEM.
KM Transferrase, Multigene family.
FT INT MET 0
FT SEQUENCE 217 AA; 25839 MW; ALEE3938F590B829 CRC64;
Query Match 70.6%; Score 36; DB 1; Length 217;
Best Local Similarity 85.7%; Pred. No. 9.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 PPNAPYL 9
Db 56 PPNAPYL 62
RESULT 11
GTML RAT STANDARD; PRT; 217 AA.
ID GTML RAT
AC P04905;
DT 13-AUG-1987 (Rel. 05, Created)

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DT 01-AUG-1988 (Rel. 08, last sequence update)  
 DT 15-SEP-2003 (Rel. 42, last annotation update)  
 DE Glutathione S-transferase Yb1 (EC 2.5.1.18) (Chain 3) (GST M1-1)  
 DE (GST class-mu 1).  
 GN GSTM1.  
 OS Rattus norvegicus (Rat).  
 CC Eumariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. (CLONE PGTR200).  
 RX MEDLINE=86312882; PubMed=2875437;  
 RA Lai H.-C.J., Grove G., Tu C.-P.D.;  
 RT "Cloning and sequence analysis of a cDNA for a rat liver glutathione  
 S-transferase Yb subunit."  
 RL Nucleic Acids Res. 14:6101-6114(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A. (CLONE PGTA/C44).  
 RX MEDLINE=86033768; PubMed=3840477;  
 RA Ding G.J.-P., Lu A.Y.H., Pickett C.B.;  
 RT "Rat liver glutathione S-transferases. Nucleotide sequence analysis  
 of a Yb1 cDNA clone and prediction of the complete amino acid  
 sequence of the Yb1 subunit."  
 RL J. Biol. Chem. 260:13268-13271(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86224097; PubMed=3011803;  
 RA Ding G.J.-P., Ding V.D.-H., Rodkey J.A., Bennett C.D., Lu A.Y.H.,  
 RA Pickett C.B.;  
 RT "Rat liver glutathione S-transferases. DNA sequence analysis of a Yb2  
 cDNA clone and regulation of the Yb1 and Yb2 mRNAs by  
 phenobarbital."  
 RL J. Biol. Chem. 261:7952-7957(1986).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87308179; PubMed=3040722;  
 RA Chang C., Saltzman A.G., Sorensen N.S., Hilpakka R.A., Liao S.;  
 RT "Identification of glutathione S-transferase Yb1 mRNA as the  
 androgen-repressed mRNA by cDNA cloning and sequence analysis."  
 RL J. Biol. Chem. 262:11901-11903(1987).  
 RN [5]  
 RP SEQUENCE OF 1-23.  
 RC STRAIN=Mistar; TISSUE=Olfactory epithelium;  
 RX MEDLINE=93277499; PubMed=8503873;  
 RA Ben-Arie N., Khen M., Lancel D.;  
 RT "Glutathione S-transferases in rat olfactory epithelium:  
 purification, molecular properties and odorant biotransformation."  
 RL Biochem. J. 292:379-384(1993).  
 RN [6]  
 RP MUTAGENESIS OF CYS-86.  
 RX MEDLINE=91354218; PubMed=1883338;  
 RA Hsieh J.-C., Huang S.-C., Chen W.-L., Lai Y.-C., Tam M.F.;  
 RT "Cysteine-86 is not needed for the enzymic activity of glutathione S-  
 transferase 3-3."  
 RL Biochem. J. 278:293-297(1991).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RX MEDLINE=93041702; PubMed=1420139;  
 RA Ji X., Zhang P., Armstrong R.N., Gilliland G.L.;  
 RT "The three-dimensional structure of a glutathione S-transferase from  
 the mu gene class. Structural analysis of the binary complex of  
 isoenzyme 3-3 and glutathione at 2.2-A resolution."  
 RL Biochemistry 31:10169-10184(1992).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RA Fu J.-H., Rose J., Tam M.F., Wang B.-C.;  
 RT "New crystal forms of a mu-class glutathione S-transferase from rat  
 liver."  
 RL Acta Crystallogr. D 50:219-224(1994).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=94153886; PubMed=8110735;  
 RA Ji X., Johnson W.W., Sesay M.A., Dickert L., Prasad S.M., Ammon H.L.,

RA Armstrong R.N., Gilliland G.L.;  
 RT "Structure and function of the xenobiotic substrate binding site of a  
 glutathione S-transferase as revealed by X-ray crystallographic  
 RT analysis of product complexes with the diastereomers of 9-(S-  
 RT glutathionyl)-10-hydroxy-9,10-dihydrophenanthrene."  
 RL Biochemistry 33:1043-1052(1994).  
 CC -1- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER  
 CC OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.  
 CC -1- FUNCTION: THE OLFACTORY GST MAY BE CRUCIAL FOR THE ACTIVITY OF THE  
 CC OLFACTORY PROCESS.  
 CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.  
 CC -1- SUBUNIT: HOMODIMER OR HETERODIMER.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- MISCELLANEOUS: RAT LIVER GLUTATHIONE S-TRANSFERASES (GST) CONSIST  
 CC OF BINARY COMBINATIONS OF THREE MAJOR CLASSES OF SUBUNITS  
 CC DESIGNATED: YA (25 KDA), YB (27 KDA) AND YC (28 KDA).  
 CC -1- MISCELLANEOUS: YB SUBCLASS SELECTIVELY BINDS STEROID HORMONES.  
 CC -1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. MU FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; X04229; CAA27811.1; -;  
 CC EMBL; M11719; AAA41287.1; -;  
 CC EMBL; J02810; AAA41293.1; -;  
 CC PIR; A29794; A29794.  
 CC PDB; 1G8B; 31-OCT-93.  
 CC PDB; 1G8C; 31-OCT-93.  
 CC PDB; 2GST; 31-OCT-93.  
 CC PDB; 3GST; 31-JAN-94.  
 CC PDB; 4GST; 31-OCT-93.  
 CC PDB; 5GST; 31-OCT-93.  
 CC PDB; 6GST; 08-NOV-96.  
 CC PDB; 6GSU; 08-NOV-96.  
 CC PDB; 6GSV; 08-NOV-96.  
 CC PDB; 6GSX; 08-NOV-96.  
 CC PDB; 6GSY; 08-NOV-96.  
 CC PDB; 5FNG; 27-JUN-99.  
 CC PDB; 3FYG; 01-JUN-99.  
 CC InterPro; IPR004046; GST\_Cterm.  
 CC InterPro; IPR003081; GST\_mu.  
 CC InterPro; IPR004045; GST\_Nterm.  
 CC Pfam; PR00043; GST\_C; 1.  
 CC Pfam; PF02798; GST\_N; 1.  
 CC PRINTS; PR01267; GSTRNSFRASEM.  
 CC Transferrase; Multigene family; 3D-structure; Olfaction.  
 CC INT MET 0  
 CC MUTAGEN 86 86 C-S: NO CHANGE IN ACTIVITY.  
 CC CONFLICT 168 168 I -> N (IN REF. 3).  
 CC CONFLICT 198 199 KS -> NC (IN REF. 2).  
 CC STRAND 2 7  
 CC TURN 11 13  
 CC HELIX 14 22  
 CC TURN 23 24  
 CC STRAND 27 32  
 CC TURN 37 39  
 CC HELIX 43 46  
 CC TURN 47 48  
 CC HELIX 49 51  
 CC STRAND 61 64  
 CC TURN 65 66  
 CC STRAND 67 70  
 CC HELIX 72 82  
 CC TURN 83 84  
 CC HELIX 90 114  
 CC TURN 115 115  
 CC TURN 117 118

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FT HELIX 119 128
FT TURN 129 129
FT HELIX 130 141
FT TURN 142 143
FT HELIX 154 169
FT TURN 171 176
FT HELIX 178 188
FT TURN 189 189
FT HELIX 191 197
FT TURN 198 198
FT TURN 200 201
FT TURN 210 211
SQ SEQUENCE 217 AA; 25782 MW; 2ACE8D49DA785118 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 217;
Best Local Similarity 85.7%; Pred. No. 9.4;
Matches 6; Conservative. 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 PPNAPYL 9
Db 56 PPNAPYL 62

RESULT 12
GTW2_HUMAN STANDARD; PRT; 217 AA.
ID P28161; Q8WWE1;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Glutathione S-transferase Mu 2 (EC 2.5.1.18) (GSTW2-2) (GST class-mu
2)
GN GSTW2 OR GST4
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=91239584; PubMed=2034681;
RT "Cloning, expression, and characterization of a class-mu glutathione
transferase from human muscle, the product of the GST4 locus."
RL Proc. Natl. Acad. Sci. U.S.A. 88:4443-4447 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carlinici P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeck S.A., McEwen P.J., McKernan K.D., Malek J.A., Gunaratne P.H.,
RA Richards S., Woley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs S.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
RX MEDLINE=94238693; PubMed=8182750;
RA Raghunathan S., Chandross R.J., Kretsinger R.H., Allison T.J.,

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RA Penington C.J., Rule G.S.;
RT "Crystal structure of human class mu glutathione transferase GSTW2-2.
RT Effects of lattice packing on conformational heterogeneity."
RL J. Mol. Biol. 238:815-832 (1994).
CC -1- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER
CC OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.
CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: THIS IS A MUSCLE ISOZYME.
CC -1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. MU FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M63509; AAA60963.1; -.
DR EMBL; BC017836; AAH17836.1; -.
DR PIR; A39375; A39375.
DR PDB; 1HNA; 31-JAN-94.
DR PDB; 1HNB; 31-JAN-94.
DR PDB; 1HNC; 31-JAN-94.
DR PDB; 2GTU; 02-MAR-99.
DR PDB; 3GTU; 29-JUL-99.
DR Genew; HGNC:4634; GSTW2.
DR MIM; 138380; -.
DR GO; GO:0004364; F:glutathione transferase activity; TAS.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR003081; GST_mu.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF00045; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
DR PRINTS; PR01267; GSTRNSFRASEM.
KW Transferase; Multigene family; 3D-structure.
FT INIT MET 0
FT CONFILCT 189 217
FT STRAND 2 7
FT HELIX 11 13
FT HELIX 14 22
FT TURN 23 24
FT STRAND 27 32
FT HELIX 43 46
FT TURN 47 48
FT HELIX 49 51
FT STRAND 61 64
FT TURN 65 66
FT STRAND 67 70
FT HELIX 72 82
FT TURN 83 84
FT HELIX 90 112
FT TURN 113 114
FT HELIX 119 141
FT STRAND 142 143
FT STRAND 146 146
FT TURN 147 148
FT STRAND 149 149
FT HELIX 154 169
FT HELIX 171 175
FT TURN 176 176
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FT HELIX 191 198
FT TURN 200 201
FT TURN 207 211
FT TURN 214 215
SQ SEQUENCE 217 AA; 25613 MW; 25603A909482CA39 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 217;

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Best Local Similarity 85.7%; Pred. No. 9.4;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 FPNAPYL 9  
Db 56 FPNAPYL 62

## RESULT 13

GT2\_MOUSE STANDARD; PRT; 217 AA.

AC P15626;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Glutathione S-transferase Mu 2 (EC 2.5.1.18) (GST class-mu 2)  
GN GSTM2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

SEQUENCE FROM N.A.

RA Townsend A.J., Goldsmith M.E., Pickett C.B., Cowan K.H.;  
RT "Isolation, characterization, and expression in *Escherichia coli* of  
two murine Mu class glutathione S-transferase cDNAs homologous to the  
rat subunits 3 (Yb1) and 4 (Yb2).";  
RL J. Biol. Chem. 264:21582-21590(1989).

RP SEQUENCE FROM N.A.

RC STRAIN=129/SVJ;  
RX MEDLINE=21297196; PubMed=11404019;  
RA Kumar A., Reddy E.P.;  
RT "Genomic organization and characterization of the promoter region of  
murine GSTM2 gene.";  
RL Gene 270:221-229(2001).

-1- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER  
OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.

-1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.

-1- SUBUNIT: Homodimer.

-1- SUBCELLULAR LOCATION: Cytoplasmic.

-1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. MU FAMILY.

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CC EMBL; J04696; AAA37706.1; -;  
DR EMBL; AF139526; AAK8508.1; -;  
DR PIR; B34159; B34159.

DR HSSP; P09488; 1GTU.  
DR SWISS-2DPAGE; P15626; MOUSE.

DR MGD; MGI:95861; Gstm2.  
DR InterPro; IPR004046; GST\_Chem.

DR InterPro; IPR003081; GST\_mu.  
DR InterPro; IPR004045; GST\_Nterm.

DR Pfam; PF00043; GST\_C; 1.  
DR Pfam; PF02798; GST\_N; 1.

DR PRINTS; PRO1267; GSTNSFRSEM.  
DR Transferase; Multigene family.

FT INIT MET 0  
SQ SEQUENCE 217 AA; 25585 MW; A3979D445FE08AE CRC64;

Query Match 70.6%; Score 36; DB 1; Length 217;  
Best Local Similarity 85.7%; Pred. No. 9.4;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 FPNAPYL 9  
Db 56 FPNAPYL 62

## RESULT 14

GT2\_RAT STANDARD; PRT; 217 AA.

AC P08010;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Glutathione S-transferase Yb2 (EC 2.5.1.18) (Chain 4) (GST class-mu  
2)  
GN GSTM2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

SEQUENCE FROM N.A.

RA Lai H.-C.J., Qian B., Grove G., Tu C.-P.D.;  
RT "Gene expression of rat glutathione S-transferases. Evidence for gene  
conversion in the evolution of the Yb multigene family.";  
RL J. Biol. Chem. 263:11389-11395(1988).

RP SEQUENCE:

RC STRAIN=Sprague-Dawley;  
RX MEDLINE=86224097; PubMed=3699019;

RA Alin P., Mannervik B., Joernvall H.;  
RT "Cytosolic rat liver glutathione transferase 4-4. Primary structure  
of the protein reveals extensive differences between homologous  
glutathione transferases of classes alpha and mu.";  
RL Eur. J. Biochem. 156:343-350(1986).

RP SEQUENCE OF 24-217 FROM N.A.

RC MEDLINE=86224097; PubMed=3011803;

RA Ding G.-F., Ding V.D.-H., Rodkey J.A., Bennett C.D., Lu A.Y.H.,  
Pickett C.B.;

RT "Rat liver glutathione S-transferases. DNA sequence analysis of a Yb2  
cDNA clone and regulation of the Yb1 and Yb2 mRNAs by  
phenobarbital.";

RL J. Biol. Chem. 261:7952-7957(1986).

RP SEQUENCE OF 32-217 FROM N.A.

RC MEDLINE=87008619; PubMed=3020050;

RA Lai H.-C.J., Tu C.-P.D.;

RT "Rat glutathione S-transferases supergene family. Characterization of  
an anionic Yb subunit cDNA clone.";

RL J. Biol. Chem. 261:13793-13799(1986).

RP SEQUENCE OF 1-21.

RC STRAIN=Wistar; Tissue=Olfactory epithelium;  
RX MEDLINE=93277499; PubMed=8503873;

RA Ben-Arie N., Khen M., Lancel D.;

RT "Glutathione S-transferases in rat olfactory epithelium:  
purification, molecular properties and odorant biotransformation.";

RL Biochem. J. 292:379-384(1993).

-1- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER  
OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.

-1- FUNCTION: THE OLFACTORY GST MAY BE CRUCIAL FOR THE ACTIVITY OF THE  
OLFACTORY PROXES.

-1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.

-1- SUBUNIT: HOMODIMER OR HETERODIMER.

-1- SUBCELLULAR LOCATION: Cytoplasmic.

-1- MISCELLANEOUS: RAT LIVER GLUTATHIONE S-TRANSFERASES (GST) CONSIST  
OF BINARY COMBINATIONS OF THREE MAJOR CLASSES OF SUBUNITS  
DESIGNATED: YA (25 KDA), YB (27 KDA) AND YC (28 KDA).  
-1- MISCELLANEOUS: YB SUBCLASS SELECTIVELY BINDS STEROID HORMONES.  
-1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. MU FAMILY.

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 CC -----  
 DR EMBL; J02592; AAA41285.1; -  
 DR EMBL; M13590; AAA42351.1; -  
 DR EMBL; J03914; AAA41296.1; -  
 DR PIR; A29231; XURTG4.  
 DR HSSP; P09488; 1GTU.  
 DR InterPro; IPR004046; GST\_Cterm.  
 DR InterPro; IPR004045; GST\_Nterm.  
 DR Pfam; PF00043; GST\_C; 1.  
 DR Pfam; PF02798; GST\_N; 1.  
 KW Transferrase; Multigene family; Olfaction.  
 FT INIT MET 0  
 FT CONFLICT 0  
 SQ SEQUENCE 217 AA; 25571 MW; F27B3D5831FF789F CRC64;  
 Query Match 70.6%; Score 36; DB 1; Length 217;  
 Best Local Similarity 85.7%; Pred. No. 9.4;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 3 FPNAPYL 9  
 Db 56 FPNAPYL 62  
 RESULT 15  
 GYM3\_MOUSE STANDARD; PRT; 217 AA.  
 ID GYM3\_MOUSE  
 AC P19639;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Glutathione S-transferase Mu 3 (EC 2.5.1.18) (GST class-mu 3)  
 DE (Glutathione S-transferase GTS.3).  
 GN GSTM3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88330838; PubMed=3417659;  
 RA Pearson W.R., Reinhardt J., Sisk S.C., Anderson K.S., Adler P.N.;  
 RT "Tissue-specific induction of murine glutathione transferase mRNAs by  
 RT butylated hydroxyanisole."  
 RL J. Biol. Chem. 263:13324-13332(1988).  
 RN [2]  
 RP SEQUENCE OF 1-40 FROM N.A.  
 RX MEDLINE=83109018; PubMed=6822548;  
 RA Pearson W.R., Windle J.J., Morrow J.F., Benson A.M., Talalay P.;  
 RT "Increased synthesis of glutathione S-transferases in response to  
 RT anticarcinogenic antioxidants. Cloning and measurement of messenger  
 RT RNA."  
 RL J. Biol. Chem. 258:2052-2062(1983).  
 RN [3]  
 RP SEQUENCE OF 1-25.  
 RX MEDLINE=86042634; PubMed=3864155;  
 RA Manervik B., Allin P., Guttenberg C., Jansson H., Tahir M.K.,  
 RA Warholm M., Joernvall H.;  
 RT "Identification of three classes of cytosolic glutathione transferase  
 RT common to several mammalian species: correlation between structural  
 RT data and enzymatic properties."  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7202-7206(1985).  
 CC -1- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER  
 CC OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.  
 CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. MU FAMILY.  
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 CC -----  
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 DR PIR; B28946; B28946.  
 DR HSSP; P04905; 2GST.  
 DR MED; MGI:106026; Gatm3.  
 DR InterPro; IPR004046; GST\_Cterm.  
 DR InterPro; IPR003081; GST\_mu.  
 DR InterPro; IPR004045; GST\_Nterm.  
 DR Pfam; PF00043; GST\_C; 1.  
 DR Pfam; PF02798; GST\_N; 1.  
 DR PRINTS; PR01267; GSTM3SFRASEM.  
 KW Transferrase; Multigene family.  
 FT INIT MET 0  
 FT CONFLICT 0  
 SQ SEQUENCE 217 AA; 25570 MW; C4D8950FEA585D8 CRC64;  
 Query Match 70.6%; Score 36; DB 1; Length 217;  
 Best Local Similarity 85.7%; Pred. No. 9.4;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 3 FPNAPYL 9  
 Db 56 FPNAPYL 62  
 Search completed: January 21, 2004, 08:45:07  
 Job time : 12 secs

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: January 21, 2004, 08:36:24 ; Search time 35 Seconds  
(without alignments)  
66.356 Million cell updates/sec

Title: US-09-625-963A-1  
Perfect score: 51  
Sequence: 1 RMPNAPYL 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	407	13	P79958 xenopus lae
2	51	100.0	446	4	O15881 homo sapien
3	47	92.2	390	13	O42223 trachemys s
4	43	84.3	386	13	O90XX8 oncorhynch
5	43	84.3	388	13	O90XX7 oncorhynch
6	43	84.3	409	13	O91657 xenopus lae
7	43	84.3	417	13	O90XX6 oncorhynch
8	41	80.4	213	16	O929M3 listeria in
9	41	80.4	213	16	O8Y5B7 listeria m
10	40	78.4	250	13	O985C4 brachydanio
11	40	78.4	289	16	O8XPG7 ralecomia s
12	40	78.4	392	13	O91030 gallus gall
13	40	78.4	414	13	O918A1 gallus gall
14	40	78.4	417	13	O918A0 gallus gall
15	40	78.4	419	13	O9PU77 brachydanio
16	39	76.5	203	16	O83076 treponema p

17	39	76.5	392	13	O91BF0	O91BF0 anguilla ja
18	39	76.5	426	13	O9W611	O9W611 cynops pyr
19	38	74.5	205	16	O91AD6	O91AD6 pseudomona
20	38	74.5	214	16	O8TSH2	O8YH2 anabaena sp
21	38	74.5	410	13	O8UIR9	O81Y9 oryzias lat
22	38	74.5	581	10	O9FE297	O91E97 arabidopsis
23	38	74.5	581	10	O8W4K7	O8W4K7 arabidopsis
24	38	74.5	662	5	O9N6S5	O9N6S5 leishmania
25	38	74.5	956	5	O961M6	O961M6 drosophila
26	38	74.5	2175	5	O9W198	O9W198 drosophila
27	37	72.5	183	16	O8D9S3	O8D9S3 vldrio vuln
28	37	72.5	444	10	O91S41	O91S41 arabidopsis
29	37	72.5	541	3	O8TG25	O8TG25 aspergillus
30	37	72.5	1160	4	O8TD24	O8TD24 homo sapien
31	36	70.6	32	11	O9QVM0	O9QVM0 mus sp. glu
32	36	70.6	37	11	O9QVM3	O9QVM3 mus sp. glu
33	36	70.6	62	10	O8GSM0	O8GSM0 tritricum ae
34	36	70.6	62	10	O8GSL8	O8GSL8 tritricum ae
35	36	70.6	82	4	O9UE37	O9UE37 homo sapien
36	36	70.6	118	4	O96BP2	O96BP2 homo sapien
37	36	70.6	181	4	O8TC98	O8TC98 homo sapien
38	36	70.6	188	6	O9WZB4	O9WZB4 capra hircu
39	36	70.6	195	4	O05465	O05465 homo sapien
40	36	70.6	218	6	O9TSM4	O9TSM4 macaca fasc
41	36	70.6	218	6	O9NOV4	O9NOV4 bos taurus
42	36	70.6	218	6	O9TSM5	O9TSM5 macaca fasc
43	36	70.6	218	11	O91Y83	O91Y83 cavia porce
44	36	70.6	218	11	O8R516	O8R516 mus musculu
45	36	70.6	218	11	O8K0C3	O8K0C3 mus musculu

## ALIGNMENTS

RESULT 1

ID P79958 PRELIMINARY; PRT; 407 AA.

AC P79958; 01-MAY-1997 (TREMBLrel. 03, Created)

DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Wtl protein.

GN Wtl.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI\_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

RX MEDLINE=97074667; PubMed=8917094;

RA Samba K., Salto-Ueno R., Takayama G., Kondo M.;

RT "CDNA cloning and its promoter-specific expression of the Wtl"

RT tumor suppressor gene, Wtl, from Xenopus laevis.";

RL Gene 175:167-172(1996).

DR EMBL; D82051; BA011522.1; -;

DR HSSP; P08046; IAA.

DR InterPro; IPR000976; Wtlms tumour.

DR InterPro; IPR007087; Znf\_C2H2.

DR Pfam; PF02165; Wtl; 1.

DR Pfam; PF00096; Zf-C2H2; 4.

DR PRINTS; PR00049; WtlmsTUMOUR.

DR PRODom; PD000003; Znf\_C2H2; 2.

DR SMART; SM00355; Znf\_C2H2; 4.

DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 4.

DR PROSITE; PS00157; ZINC\_FINGER\_C2H2\_2; 4.

KW Metal-binding; Zinc; Zinc-finger.

SQ SEQUENCE 407 AA; 45983 MW; E2554C658005870C CRC64;

Query Match 100.0%; Score 51; DB 13; Length 407;

Best local Similarity 100.0%; Pred. No. 0.15;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
 Db 107 RMFPNAPYL 115

RESULT 2  
 Q15881 PRELIMINARY; PRT; 446 AA.  
 ID Q15881  
 AC Q15881  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Wilms tumor gene 1, exon 1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=9224183; PubMed=1572653;  
 RA Gesseler M., Konig A., Bruns G.A.;  
 RT "The genomic organization and expression of the WT1 gene.";  
 RL Genomics 12:807-813(1992).  
 DR EMBL; X61631; CAA43819.1; JOINED.  
 DR EMBL; X61632; CAA43819.1; JOINED.  
 DR EMBL; X61633; CAA43819.1; JOINED.  
 DR EMBL; X61634; CAA43819.1; JOINED.  
 DR EMBL; X61635; CAA43819.1; JOINED.  
 DR EMBL; X61636; CAA43819.1; JOINED.  
 DR EMBL; X61637; CAA43819.1; JOINED.  
 DR EMBL; X61638; CAA43819.1; JOINED.  
 DR HSSP; P08046; 1AAY.  
 DR InterPro; IPR000976; Wilms\_tumour.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR Pfam; PF02165; WT1; 1.  
 DR Pfam; PF00096; zf-C2H2; 4.  
 DR PRINTS; PR00049; WILMSTUMOUR.  
 DR PRODOM; PD000003; Znf\_C2H2; 2.  
 DR SMART; SM00355; Znf\_C2H2; 4.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 4.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 4.  
 KW Metal-binding; Zinc; Zinc-finger.  
 SQ SEQUENCE 446 AA; 48842 MW; 8CB7FC04F41CFC64; CRC64;

Query Match 100.0%; Score 51; DB 4; Length 446;  
 Best Local Similarity 100.0%; Pred. No. 0.16;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
 Db 126 RMFPNAPYL 134

RESULT 3  
 O42223 PRELIMINARY; PRT; 390 AA.  
 ID O42223  
 AC O42223  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Wilms tumor 1 protein.  
 GN TWI1.  
 OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Testudines; Cryptodira; Testudinoidae; Emydidae; Trachemys.  
 NCBI\_TaxID=34903;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP Spotila L.D., Hall S.E.;  
 RT "Expression of a new RNA-splice isoform of WT1 in developing kidney/gonadal complexes of the turtle, Trachemys scripta.";  
 RT Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF019779; AAB70832.1; --  
 DR HSSP; P08046; 1AAY.  
 DR InterPro; IPR000976; Wilms\_tumour.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR Pfam; PF02165; WT1; 1.  
 DR Pfam; PF00096; zf-C2H2; 4.  
 DR PRINTS; PR00049; WILMSTUMOUR.  
 DR PRODOM; PD000003; Znf\_C2H2; 2.  
 DR SMART; SM00355; Znf\_C2H2; 4.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 3.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 4.  
 KW Metal-binding; Zinc; Zinc-finger.  
 SQ SEQUENCE 390 AA; 43620 MW; 1C9987435BE927C2 CRC64;

Query Match 92.2%; Score 47; DB 13; Length 390;  
 Best Local Similarity 88.9%; Pred. No. 0.81;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
 Db 109 RMFPNAPYL 117

RESULT 4  
 Q90XX8 PRELIMINARY; PRT; 386 AA.  
 ID Q90XX8  
 AC Q90XX8  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Wilms' tumor suppressor 1a.  
 GN WT-T1A.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Procaranthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 NCBI\_TaxID=8022;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=21337607; PubMed=11444705;  
 RA Brune111 J.P., Robison B.D., Thorgaard G.H.;  
 RT "Ancient and recent duplications of the rainbow trout Wilms' tumor gene.";  
 RL Genome 44:455-462(2001).  
 DR EMBL; AF334670; AAKS2719.1; --  
 DR InterPro; IPR000976; Wilms\_tumour.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR Pfam; PF02165; WT1; 1.  
 DR Pfam; PF00096; zf-C2H2; 4.  
 DR PRINTS; PR00049; WILMSTUMOUR.  
 DR PRODOM; PD000003; Znf\_C2H2; 2.  
 DR SMART; SM00355; Znf\_C2H2; 4.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 4.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 4.  
 KW Metal-binding; Zinc; Zinc-finger.  
 SQ SEQUENCE 386 AA; 43286 MW; 05622EF642FC9B5 CRC64;

Query Match 84.3%; Score 43; DB 13; Length 386;  
 Best Local Similarity 88.9%; Pred. No. 4.6;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
 Db 112 RMFPNAPYL 120

RESULT 5  
 Q90XX7 PRELIMINARY; PRT; 388 AA.  
 ID Q90XX7  
 AC Q90XX7  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)



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DE Wlms' tumor suppressor 1b.
GN WT-TLB.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21337607; PubMed=11444705;
RT Brunelli J.P., Robison B.D., Thorgaard G.H.;
RT "Ancient and recent duplications of the rainbow trout Wlms' tumor
RT gene.";
RL Genome 44:455-462(2001).
DR EMBL; AF344671; AAKS2720.1; -.
DR InterPro; IPR000976; Wlms_tumour.
DR Pfam; PF02165; WT1; 1.
DR Pfam; PF00096; zfc_C2H2; 4.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
KM Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 388 AA; 43398 MW; BC92266DE745DFCC CRC64;

Query Match      84.3%; Score 43; DB 13; Length 388;
Best Local Similarity 88.9%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9
Db 112 RMFSNAPYL 120

RESULT 6
Q91657 PRELIMINARY; PRT; 409 AA.
AC Q91657;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Wlms' tumor suppressor (WT1).
GN WT1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX Carroll T.J., Vize P.D.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 289-370 FROM N.A.
RC TISSUE=Mesonephros;
RX MEDLINE=9606905; PubMed=7478606;
RA Kent J., Coriat A.M., Sharpe P.T., Hastie N., Van Heyningen V.;
RA "The evolution of WT1 sequence and expression pattern in the
RT vertebrates.";
RL Oncogene 11:1781-1792(1995).
DR EMBL; U42011; AAB53152.1; -.
DR EMBL; X85733; CA59738.1; -.
DR HSSP; P08046; IAAV.
DR InterPro; IPR000976; Wlms_tumour.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF02165; WT1; 1.
DR Pfam; PF00096; zfc_C2H2; 4.
DR PRINTS; PR00049; WLMSTUMOUR.
DR PRODOM; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
KM Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 417 AA; 46557 MW; 5217620CD41D030 CRC64;

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KM Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 409 AA; 46186 MW; 2217FC04612CDE10 CRC64;

Query Match      84.3%; Score 43; DB 13; Length 409;
Best Local Similarity 88.9%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9
Db 106 RMFSNAPYL 114

RESULT 7
Q90XX6 PRELIMINARY; PRT; 417 AA.
AC Q90XX6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Wlms' tumor suppressor 1b variant.
GN WT-TLB.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21337607; PubMed=11444705;
RT Brunelli J.P., Robison B.D., Thorgaard G.H.;
RT "Ancient and recent duplications of the rainbow trout Wlms' tumor
RT gene.";
RL Genome 44:455-462(2001).
DR EMBL; AF344672; AAKS2721.1; -.
DR InterPro; IPR000976; Wlms_tumour.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF02165; WT1; 1.
DR Pfam; PF00096; zfc_C2H2; 4.
DR PRINTS; PR00049; WLMSTUMOUR.
DR PRODOM; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
KM Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 417 AA; 46557 MW; 5217620CD41D030 CRC64;

Query Match      84.3%; Score 43; DB 13; Length 417;
Best Local Similarity 88.9%; Pred. No. 4.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9
Db 112 RMFSNAPYL 120

RESULT 8
Q929M3 PRELIMINARY; PRT; 213 AA.
AC Q929M3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein lin2252.
GN LIN2252.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CLIP 11262 / Serovar 6a;
RX PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Ruaniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,

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RA Charbit A., Cherouani F., Couve E., de Daruvar A., Deloux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunz F., Kurapkak G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Rammel B., Rose M., Schueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehlant J., Cossart P.,
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL: AL596171; CAC97480.1; -.
DR Listlist: LIT02252; -.
KM Hypothetical protein, Complete proteome.
SQ SEQUENCE 213 AA; 25341 MW; B87F90FD1D1F0E78 CRC64;

Query Match
Best Local Similarity 80.4%; Score 41; DB 16; Length 213;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FPNAPYL 9
Db 67 FPNAPYL 73

RESULT 9
ID Q8Y5B7 PRELIMINARY; PRT; 213 AA.
AC Q8Y5B7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein lmo2148.
GN LMO2148.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusnok C., Amend A.,
RA Baquero F., Berche P., Blocker H., Brandt P., Chakraborty T.,
RA Chabib A., Cherouani F., Couve E., de Daruvar A., Deloux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunz F., Kurapkak G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Rammel B., Rose M., Schueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehlant J., Cossart P.,
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL: AL591982; CAD00226.1; -.
DR Listlist: LMO02148; -.
KM Hypothetical protein, Complete proteome.
SQ SEQUENCE 213 AA; 25361 MW; A95F9363E2F0E78 CRC64;

Query Match
Best Local Similarity 100.0%; Score 41; DB 16; Length 213;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FPNAPYL 9
Db 67 FPNAPYL 73

RESULT 10
ID Q98SJ4 PRELIMINARY; PRT; 250 AA.
AC Q98SJ4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)

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DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Wt1s tumor suppressor (Fragment).
GN Wt1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Serruca F.C., Fishman M.C.;
RT "Pre-pattern in the pronephric kidney field of zebrafish.";
RL Development 0:0-0(2001).
DR EMBL: AY028627; AAK27262.1; -.
DR ZFIN; ZDB-GENE-980526-558; Wt1.
DR InterPro; IPR000976; Wt1s_tumour.
DR Pfam; PF02165; Wt1; 1.
FT NON_TER 1 1
FT NON_TER 250 250
SQ SEQUENCE 250 AA; 27236 MW; 90FA4B05F59F6A CRC64;

Query Match
Best Local Similarity 78.4%; Score 40; DB 13; Length 250;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFNPAPYL 9
Db 88 MFNSNPYL 96

RESULT 11
ID Q8XP67 PRELIMINARY; PRT; 289 AA.
AC Q8XP67;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical lipoprotein transmembrane protein Rsp1673.
GN RSP1673 OR RS02232.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Ralstonia solanacearum.
OG Plasmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangesot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Catolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cumac S., Demange N.,
RA Gaepin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL: AL646086; CAD18824.1; -.
KM Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 289 AA; 29665 MW; 715867B3C03C9BC CRC64;

Query Match
Best Local Similarity 78.4%; Score 40; DB 16; Length 289;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MFNPAPYL 9
Db 115 MLNPAPYL 122

RESULT 12
ID Q91030 PRELIMINARY; PRT; 392 AA.
AC Q91030;
DT 091030

```

AC 091030;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-MAY-2003 (TReMBLrel. 23, Last annotation update)  
 DE Chick wilm's tumour protein (Fragment).  
 GN CWT1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RX MEDLINE=96088905; PubMed=7478606;  
 RA Kent J., Coriat A.M., Sharpe P.T., Hastie N., van Heyningen V.;  
 RT "The evolution of WT1 sequence and expression in the vertebrates";  
 RL Oncogene 11:1781-1792(1995).  
 DR EMBL; X85731; CA59736.1; -.  
 DR HSSP; P08046; 1AIG.  
 DR InterPro; IPR000976; Wt1ms tumour.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR Pfam; PF02165; WT1; 1.  
 DR Pfam; PF00096; zf-C2H2; 3.  
 DR PRINTS; PR00049; WILMSTUMOUR.  
 DR PRODOM; PD000003; Znf\_C2H2; 2.  
 DR SMART; SM00355; Znf\_C2H2; 3.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 3.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 3.  
 KM Metal-binding; Zinc; Zinc-finger.  
 FT NOW TER 392  
 SQ SEQUENCE 392 AA; 43869 MW; 761F0D350E4EDBF CRC64;

Query Match 78.4%; Score 40; DB 13; Length 392;  
 Best Local Similarity 77.8%; Pred. No. 17;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
 Db 109 RMFPQRPYL 117

RESULT 13  
 ID 0918A1 PRELIMINARY; PRT; 414 AA.  
 AC 0918A1;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE WT1(-KTS) protein.  
 GN WT1(-KTS).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RX [1]  
 RA SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RT "Chicken counterpart of Wt1ms' tumor suppressor gene 1.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB033633; BAA94793.1; -.  
 DR HSSP; P08046; 1AAY.  
 DR InterPro; IPR000976; Wt1ms tumour.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR Pfam; PF02165; WT1; 1.  
 DR Pfam; PF00096; zf-C2H2; 4.  
 DR PRINTS; PR00049; WILMSTUMOUR.  
 DR PRODOM; PD000003; Znf\_C2H2; 2.  
 DR SMART; SM00355; Znf\_C2H2; 4.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 4.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 4.  
 KM PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 4.

KM Metal-binding; Zinc; Zinc-finger.  
 SQ SEQUENCE 414 AA; 46641 MW; 17B22F9B428A2EF CRC64;

Query Match 78.4%; Score 40; DB 13; Length 414;  
 Best Local Similarity 77.8%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
 Db 109 RMFPQRPYL 117

## RESULT 14

ID 0918A0 PRELIMINARY; PRT; 417 AA.  
 AC 0918A0;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE WT1(+KTS) protein.  
 GN WT1(+KTS).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RX [1]  
 RA SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RT "Chicken counterpart of Wt1ms' tumor suppressor gene 1.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB033634; BAA94794.1; -.  
 DR HSSP; P08046; 1AAY.  
 DR InterPro; IPR000976; Wt1ms tumour.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR Pfam; PF02165; WT1; 1.  
 DR Pfam; PF00096; zf-C2H2; 4.  
 DR PRINTS; PR00049; WILMSTUMOUR.  
 DR PRODOM; PD000003; Znf\_C2H2; 2.  
 DR SMART; SM00355; Znf\_C2H2; 4.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 4.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 4.  
 KM Metal-binding; Zinc; Zinc-finger.  
 SQ SEQUENCE 417 AA; 46957 MW; 47BBF7F6448F76C CRC64;

Query Match 78.4%; Score 40; DB 13; Length 417;  
 Best Local Similarity 77.8%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
 Db 109 RMFPQRPYL 117

## RESULT 15

ID 09PUT7 PRELIMINARY; PRT; 419 AA.  
 AC 09PUT7;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE Wt1ms' tumor suppressor.  
 GN Wt1.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OC NCBI\_TaxID=7955;  
 RX [1]  
 RA SEQUENCE FROM N.A.  
 RC Smith S.I., Down M., Power M., Boyd A.W.;  
 RT "Isolation and characterization of a cDNA encoding zebrafish (Danio

RT rerio) WT-1";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF144550; AAF00123.1; -.  
DR HSSP; P08046; 1AAY.  
DR ZFIN; ZDB-GENE-980526-558; WT1.  
DR InterPro; IPR000976; Wt1ms tumour.  
DR InterPro; IPR007087; Znf\_C2H2.  
DR Pfam; PF02165; WT1; 1.  
DR Pfam; PF00096; Zf-C2H2; 4.  
DR PRINTS; PR00049; WILMSTUMOUR.  
DR ProDom; PD000003; Znf\_C2H2; 2.  
DR SMART; SM00355; Znf\_C2H2; 4.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 4.  
DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 4.  
KW Metal-binding; Zinc; Zinc-finger.  
SQ SEQUENCE 419 AA; 46925 MW; 606ADFEDA619ECD CRC64;

Query Match 78.4%; Score 40; DB 13; Length 419;  
Best Local Similarity 77.8%; Pred. No. 18;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
|||:||||  
Db 111 RMFSNSPYL 119

Search completed: January 21, 2004, 08:44:10  
Job time : 37 secs



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XX OS Homo sapiens.
XX PN WO200026249-A1.
XX PD 11-MAY-2000.
XX PF 02-NOV-1999; 99WO-GB03572.
XX PR 02-NOV-1998; 98GB-0023897.
XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX PI Steaus HJ, Gao L;
XX DR WPI; 2000-376123/32.
XX PT Novel peptides comprising WT-1 and GATA-1 epitopes, their fragments or
XX PS variants, useful as vaccines for cancer immunotherapy -
XX PS Claim 1; Page 74; 93pp; English.
XX CC The present sequence is peptide epitope WT126-34, produced by WT1
XX CC expressing cells and found at residues 126-134 of the WT1 protein, which
XX CC is recognised by cytotoxic T lymphocytes. WT1 is aberrantly expressed in
XX CC leukaemia, breast cancer, melanoma and ovarian cancer. The peptide can
XX CC be used as a vaccine to stimulate the elimination, by cytotoxic T
XX CC lymphocytes, of cancer cells aberrantly expressing WT1. In addition, the
XX CC nucleic acid encoding the peptide may also be used in the same manner.
XX CC Alternatively, the peptide may be used in vitro to produce activated
XX CC cytotoxic T lymphocytes.
XX SQ Sequence 9 AA;
XX
XX Query Match 100.0%; Score 51; DB 21; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RMFPNAPYL 9
Db 1 RMFPNAPYL 9

```

RESULT 2  
AA98670 ID AAY98670 standard; Peptide; 9 AA.  
AC AAY98670;  
XX  
DT 31-JUN-2000 (first entry)  
DE WT1 derived immunogenic peptide SEQ ID NO:185.  
XX  
XX WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;  
XX metastatic disease; mouse; human; Wilm's tumour; immune response;  
XX vaccine.  
XX  
XX Homo sapiens.  
XX OS  
XX PN WO200018795-A2.  
XX PD 06-APR-2000.  
XX PF 30-SEP-1999; 99WO-US22819.  
XX PR 30-SEP-1998; 98US-0164223.  
XX PR 25-MAR-1999; 99US-0276484.  
XX PA (CORI-) CORIXA CORP.  
XX PA (GAIG/) GAIGER A.  
XX PI Gaiger A, Cheever M;  
XX

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DR PF WPI; 2000-293107/25.
XX PT Novel polypeptides comprising an immunogenic portion of a native WT1
XX PT polypeptide, useful for inhibiting the development of malignant
XX PT diseases associated with WT1 expression e.g. leukemia or cancer -
XX PS Claim 4; Page 171; 193pp; English.
XX CC The present invention describes polypeptides (I) comprising an
XX CC immunogenic portion of a native Wilm's Tumour gene product polypeptide,
XX CC WT1, (or variants of the immunogenic portion retaining the ability to
XX CC react with WT1-specific antisera and/or T-cell lines or clones) and
XX CC comprising 16 consecutive amino acids (aa) or less of a native WT1
XX CC polypeptide. The polypeptides are useful therapeutically and to
XX CC manufacture medicaments for enhancing/inducing an immune response in
XX CC patients. The polypeptides, mimetics or polynucleotides can be included
XX CC with a carrier/excipient in pharmaceutical compositions or with a
XX CC non-specific immune response enhancer (e.g. an adjuvant or enhancer
XX CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical
XX CC compositions and vaccines can be administered to human patients to
XX CC enhance or induce an immune response specific for WT1 or a cell
XX CC expressing WT1, useful to inhibit the development of malignant diseases
XX CC associated with WT1 expression, e.g. leukemia (especially acute/chronic
XX CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
XX CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma).
XX CC AAY98501 to AAY98811 represent polypeptide sequences, and AAY13848 to
XX CC AAY13862 represent PCR primers, used in the exemplification of the
XX CC present invention.
XX SQ Sequence 9 AA;
XX
XX Query Match 100.0%; Score 51; DB 21; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RMFPNAPYL 9
Db 1 RMFPNAPYL 9

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RESULT 3  
AA98778 ID AAY98778 standard; Peptide; 9 AA.  
AC AAY98778;  
XX  
DT 31-JUN-2000 (first entry)  
DE WT1 derived immunogenic peptide SEQ ID NO:293.  
XX  
XX WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;  
XX metastatic disease; mouse; human; Wilm's tumour; immune response;  
XX vaccine.  
XX  
XX Mus musculus.  
XX OS  
XX PN WO200018795-A2.  
XX PD 06-APR-2000.  
XX PF 30-SEP-1999; 99WO-US22819.  
XX PR 30-SEP-1998; 98US-0164223.  
XX PR 25-MAR-1999; 99US-0276484.  
XX PA (CORI-) CORIXA CORP.  
XX PA (GAIG/) GAIGER A.  
XX PI Gaiger A, Cheever M;  
XX  
XX WPI; 2000-293107/25.  
XX  
XX Novel polypeptides comprising an immunogenic portion of a native WT1

PT polypeptide, useful for inhibiting the development of malignant  
 PT diseases associated with WT1 expression e.g. leukemia or cancer  
 XX  
 PS Claim 4, Page 186, 193pp, English.  
 XX  
 CC The present invention describes polypeptides (I) comprising an  
 CC immunogenic portion of a native Wilms' Tumour gene product polypeptide,  
 CC WT1, (or variants of the immunogenic portion retaining the ability to  
 CC react with WT1-specific antisera and/or T-cell lines or clones) and  
 CC comprising 16 consecutive amino acids (aa) or less of a native WT1  
 CC polypeptide. The polypeptides are useful therapeutically and to  
 CC manufacture medicaments for enhancing/inducing an immune response in  
 CC patients. The polypeptides, mimetics or polynucleotides can be included  
 CC with a carrier/excipient in pharmaceutical compositions or with a  
 CC non-specific immune response enhancer (e.g. an adjuvant or enhancer  
 CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical  
 CC compositions and vaccines can be administered to human patients to  
 CC enhance or induce an immune response specific for WT1 or a cell  
 CC expressing WT1, useful to inhibit the development of malignant diseases  
 CC associated with WT1 expression, e.g. leukemia (especially acute/chronic  
 CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially  
 CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma).  
 CC AAY98501 to AAY98811 represent polypeptide sequences, and AAA13848 to  
 CC AAA13862 represent PCR primers, used in the exemplification of the  
 CC present invention.  
 XX  
 SQ Sequence 9 AA;  
 XX  
 Query Match 100.0%; Score 51; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 RMPFNAPYL 9  
 Db 1 RMPFNAPYL 9  
 XX  
 RESULT 4  
 AAY80200  
 ID AAY80200 standard; Peptide; 9 AA.  
 XX  
 AC AAY80200;  
 XX  
 DT 24-MAY-2000 (first entry)  
 XX  
 DE Human Wilms' tumour suppressor gene WT1 product peptide SEQ ID NO.5.  
 XX  
 KW Wilms' tumour suppressor gene; WT1; cancer; antigen; vaccine; MHC;  
 KW major histocompatibility complex; leukaemia; tumour; antitumour.  
 XX  
 OS Homo sapiens.  
 OS  
 XX WO200006602-A1.  
 PN  
 XX 10-FEB-2000.  
 PD  
 XX 30-JUL-1999; 99WO-JP04130.  
 PF  
 XX 31-JUL-1998; 98JP-0218093.  
 PR  
 XX (SUGI/) SUGIYAMA H.  
 PA  
 XX Sugiyama H, Oka Y;  
 PI  
 XX WPI; 2000-195264/17.  
 DR  
 XX Cancer antigens based on Wilms' tumor suppressor gene WT1 product or  
 PT peptide derivatives, for cancer vaccines in treating leukemia and solid  
 PT tumors e.g. stomach cancer, skin cancer, lung cancer and breast cancer  
 XX  
 PS Claim 5; Page 18; 48pp; Japanese.  
 XX  
 CC The present invention describes a cancer antigen containing the active

CC component of Wilms' tumour suppressor gene WT1 product, or partial  
 CC peptides, for cancer vaccines in treating leukaemia and solid tumours.  
 CC The cancer antigens are useful for cancer vaccines in treating  
 CC leukaemia, bone-marrow abnormal formation syndrome, malignant lymphoma,  
 CC multiple myeloma, stomach cancer, cancer of the large intestine, lung  
 CC cancer, breast cancer, blastoma, liver cancer, skin cancer, bladder  
 CC cancer, prostate cancer, uterus cancer, cervical cancer, or ovary  
 CC cancer. The present sequence represents a peptide from the human  
 CC Wilms' tumour suppressor gene WT1 product.  
 XX  
 SQ Sequence 9 AA;  
 XX  
 Query Match 100.0%; Score 51; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 RMPFNAPYL 9  
 Db 1 RMPFNAPYL 9  
 XX  
 RESULT 5  
 AAU68769  
 ID AAU68769 standard; Peptide; 9 AA.  
 XX  
 AC AAU68769;  
 XX  
 DT 16-JAN-2002 (first entry)  
 XX  
 DE Human Wilms' tumour protein, WT1, antigenic peptide #164.  
 XX  
 KW Human Wilms' tumour; WT1; pleural mesothelioma; antigen;  
 KW leukaemia; acute myeloid leukaemia; ALL; chronic myeloid leukaemia; CML;  
 KW acute lymphocytic leukaemia; ALL; myelodysplastic syndromes;  
 KW myeloproliferative syndrome; cancer; cytostatic.  
 XX  
 OS Homo sapiens.  
 OS  
 XX WO200162920-A2.  
 PN  
 XX 30-AUG-2001.  
 PD  
 XX 22-FEB-2001; 2001WO-US05702.  
 PF  
 XX 22-FEB-2000; 2000US-184070P.  
 PR  
 XX (CORI-) CORIXA CORP.  
 PA  
 XX Cheever MA, Gaiger A;  
 PI  
 XX WPI; 2001-648218/74.  
 DR  
 XX Composition for the treatment of mesothelioma comprises specific  
 PT peptides i.e. Wilms' tumour antigen polypeptide derived antigenic  
 PT fragments -  
 XX  
 PS Claim 1; Page 176; 242pp; English.  
 PS  
 XX The invention relates to the use of a composition comprising at least a  
 CC first isolated peptide, of between 9 and 40 amino acids or a first  
 CC nucleic acid, encoding the peptide, in the manufacture of a medicament  
 CC for treating or preventing mesothelioma. The peptides are antigenic  
 CC peptides derived from the Wilms' tumour protein WT1. The composition is  
 CC useful for the treatment of mesothelioma, Wilms' tumour, preferably  
 CC pleural mesothelioma and other WT1 associated malignancies e.g.  
 CC leukaemia (including acute myeloid leukaemia, ALL, chronic myeloid  
 CC leukaemia, CML, acute lymphocytic leukaemia, ALL, and childhood ALL),  
 CC myelodysplastic syndromes, myeloproliferative syndromes and cancers  
 CC (e.g. breast, testicular, prostate, lung and ovarian) in mammals,  
 CC preferably humans. The present sequence is an antigenic peptide of  
 CC the invention derived from human WT1.  
 XX  
 SQ Sequence 9 AA;  
 XX

Query Match 100.0%; Score 51; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9  
 |||||  
 DB 1 RMPFNAPYL 9

RESULT 6  
 AAU68877  
 ID AAU68877 standard; Peptide; 9 AA.

AC AAU68877;  
 DT 16-JAN-2002 (first entry)

DE Mouse Wilm's tumour protein, WT1, antigenic peptide #46.

XX Mouse; Wilms' tumour; WT1; pleural mesothelioma; antigen;  
 KW leukaemia; acute myeloid leukaemia; ALL; chronic myeloid leukaemia; CML;  
 KM acute lymphocytic leukaemia; ALL; myelodysplastic syndromes;  
 KM myeloproliferative syndrome; cancer; cytostatic.

XX Mus musculus.

XX WO200162920-A2.

XX 30-AUG-2001.

XX 22-FEB-2001; 2001WO-US05702.

XX 22-FEB-2000; 2000US-184070P.

XX (CORI-) CORIXA CORP.

XX Cheever MA, Gaiger A;

XX WPI; 2001-648218/74.

PT Composition for the treatment of mesothelioma comprises specific  
 PT peptides i.e. Wilms' tumour antigen polypeptide derived antigenic  
 PT fragments -

PS Claim 1; Page 24; 242pp; English.

XX The invention relates to the use of a composition comprising at least a  
 CC first isolated peptide, of between 9 and 40 amino acids or a first  
 CC nucleic acid, encoding the peptide, in the manufacture of a medicament  
 CC for treating or preventing mesothelioma. The peptides are antigenic  
 CC peptides derived from the Wilms' tumour protein WT1. The composition is  
 CC useful for the treatment of mesothelioma, Wilms' tumour, preferably  
 CC pleural mesothelioma and other WT1 associated malignancies e.g.  
 CC leukaemia (including acute myeloid leukaemia, ALL, chronic myeloid  
 CC leukaemia, CML, acute lymphocytic leukaemia, ALL, and childhood ALL),  
 CC myelodysplastic syndromes, myeloproliferative syndromes and cancers  
 CC (e.g. breast, testicular, prostate, lung and ovarian) in mammals,  
 CC preferably humans. The present sequence is an antigenic peptide of  
 CC the invention derived from mouse WT1.

XX Sequence 9 AA;

Query Match 100.0%; Score 51; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9  
 |||||  
 DB 1 RMPFNAPYL 9

RESULT 7

AA62002  
 ID AA62002 standard; Peptide; 9 AA.

XX AA62002;  
 DT 06-JUL-2001 (first entry)

DE Human WT1 immunogenic peptide SEQ ID NO: 185.

XX Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;  
 KW chromosome 11p13; zinc finger transcription factor.

XX Homo sapiens.

XX WO200125273-A2.

XX 12-APR-2001.

XX 04-OCT-2000; 2000WO-US27465.

XX 04-OCT-1999; 99US-0157459.

XX (CORI-) CORIXA CORP.

XX Skeiky YAW, Xu J, Cheever MA, Reed SG;

XX WPI; 2001-328324/34.

PT Polypeptide comprising part of the Wilm's Tumour gene product sequence is  
 PT used in the diagnosis and treatment of malignant diseases e.g. leukemia  
 PT and cancer associated with WT1 -

PS Claim 4; Page 183; 228pp; English.

XX The present invention describes compositions comprising peptides derived  
 CC from the Wilm's tumour protein WT1 and methods for their use in treating  
 CC malignant diseases. Peptides derived from both the murine and human WT1  
 CC proteins are provided. The human WT1 gene is found on chromosome 11p13,  
 CC and the protein was shown to be a zinc finger transcription factor. The  
 CC immunogenic peptides of the invention are particularly useful in the  
 CC diagnosis and treatment of cancer and leukaemia. The present sequence is  
 CC a polypeptide described in the exemplification of the invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 51; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMPFNAPYL 9  
 |||||  
 DB 1 RMPFNAPYL 9

RESULT 8  
 AA62110  
 ID AA62110 standard; Peptide; 9 AA.

XX AA62110;

XX 06-JUL-2001 (first entry)

DE Mouse WT1 immunogenic peptide SEQ ID NO: 293.

XX Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;  
 KW chromosome 11p13; zinc finger transcription factor.

XX Mus musculus.

XX WO200125273-A2.

XX 12-APR-2001.



PF 04-OCT-2000; 2000WO-US27465.  
XX  
PR 04-OCT-1999; 99US-0157459.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Skelky YAW, Xu J, Cheever MA, Reed SG;  
XX WPI; 2001-328324/34.  
DR  
XX Polypeptide comprising part of the Wilm's Tumour gene product sequence is  
PT used in the diagnosis and treatment of malignant diseases e.g. leukemia  
PT and cancer associated with WTI -  
XX  
PS Claim 4; Page 200; 228pp; English.  
XX  
CC The present invention describes compositions comprising peptides derived  
CC from the Wilm's tumour protein WTI and methods for their use in treating  
CC malignant diseases. Peptides derived from both the murine and human WTI  
CC proteins are provided. The human WTI gene is found on chromosome 11p13,  
CC and the protein was shown to be a zinc finger transcription factor. The  
CC immunogenic peptides of the invention are particularly useful in the  
CC diagnosis and treatment of cancer and leukaemia. The present sequence is  
CC a polypeptide described in the exemplification of the invention.  
XX  
SQ Sequence 9 AA;  
Query Match 100.0%; Score 51; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RMFPNAPYL 9  
DB 1 RMFPNAPYL 9  
RESULT 9  
ABG79100  
ID ABG79100 standard; Peptide; 9 AA.  
XX  
AC ABG79100;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Human WTI class I HLA widely expressed antigen peptide #1.  
XX  
XX Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;  
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;  
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;  
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;  
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;  
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;  
KW cytostatic; human.  
XX  
OS Homo sapiens.  
XX  
PN WO200264057-A2.  
XX  
PD 22-AUG-2002.  
XX  
PF 15-FEB-2002; 2002WO-US05212.  
XX  
PR 15-FEB-2001; 2001US-268687P.  
XX  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX  
PI Wang R;  
XX  
DR WPI; 2002-627577/67.  
XX  
PT Novel composition for treating a disease in an animal, comprises an  
PT immune effector cell and cell penetrating peptide associated with an  
PT antigen or antibody -

XX  
PS Disclosure; Page 19; 61pp; English.  
XX  
CC The invention relates to a composition (I) comprising an immune effector  
CC cell and a cell penetrating peptide (CPP) associated with an antigen or  
CC antibody. Also included are (1) a vaccine comprising (I), CPP  
CC associated with an antigen, and a pharmaceutically acceptable carrier  
CC and (2) preparing a composition for a disease, by providing (I)  
CC and CPP associated with an antigen for disease, and introducing the  
CC antigen-associated CPP to (I), where antigen enters into the cell.  
CC The antigens are, for example, tumour antigen derived epitopes  
CC recognised by tumour infiltrating lymphocytes (TIL) of HLA (human  
CC leukocyte antigen) class I or II. The composition is useful for enhancing  
CC immunity in an animal to a disease, by administering a mature dendritic  
CC cell comprising CPP associated with an antigen to disease, to the animal,  
CC such that following the administration, animal is protected from disease,  
CC where the animal comprises both CD4+ and CD8+ T cells. It is also useful  
CC for treating a disease (e.g. cancer, tumour, melanoma, thymoma,  
CC lymphoma, sarcoma, lung cancer, non-Hodgkin's lymphoma, leukaemia,  
CC Hodgkin's lymphoma, uterine cancer, cervical cancer, bladder cancer,  
CC kidney cancer, adenocarcinoma, breast cancer, prostate cancer,  
CC ovarian cancer and pancreatic cancer). The animal is further subjected to  
CC a cancer treatment including surgery, radiation, chemotherapy or gene  
CC therapy. The administration of (I), preferably dendritic cell is prior  
CC to, subsequent to or concurrent with, the cancer treatment. The present  
CC sequence is a tumour antigen derived epitope for inclusion in the  
CC composition of the invention.  
XX  
SQ Sequence 9 AA;  
Query Match 100.0%; Score 51; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RMFPNAPYL 9  
DB 1 RMFPNAPYL 9  
RESULT 10  
ABG33239  
ID ABG33239 standard; Peptide; 9 AA.  
XX  
AC ABG33239;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human WTI immunogenic peptide #162.  
XX  
XX Human; mouse; cytostatic; immunostimulant; WTI; cancer;  
KW immune response.  
XX  
OS Homo sapiens.  
XX  
PN WO200228414-A1.  
XX  
PD 11-APR-2002.  
XX  
PF 03-OCT-2001; 2001WO-US31139.  
XX  
PR 06-OCT-2000; 2000US-0684361.  
XX  
PR 09-OCT-2000; 2000US-0685830.  
XX  
PR 15-FEB-2001; 2001US-0785019.  
XX  
PR 24-AUG-2001; 2001US-0938864.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI (GAIG/) GAIGER A.  
XX  
DR Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;  
XX Sleath PR, Mosman S, Evans L, Spies AG, Boydston J;  
XX WPI; 2002-352217/38.  
XX

PT Novel isolated WTI polynucleotide, and encoded polypeptide, useful for  
 PT treating and diagnosing cancer in a patient -

XX Example 4; Page 194; 260pp; English.

XX The invention relates to an isolated WTI polynucleotide (I) and  
 CC polypeptide encoded by (I). The WTI polynucleotides and polypeptides  
 CC are used for treating and detecting cancer in a patient, and for  
 CC stimulating an immune response in patient. ABG33070-ABG33405  
 CC represent WTI amino acid sequences of the invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 51; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9  
 Db 1 RMPFNAPYL 9

RESULT 11

ABG33347  
 ID ABG33347 standard; peptide; 9 AA.

AC ABG33347;

DT 15-JUL-2002 (first entry)

DE Mouse WTI immunogenic peptide #44.

KW Human; mouse; cytostatic; immunostimulant; WTI; cancer;  
 KW immune response.

OS Mus musculus.

PN WO200228414-A1.

PD 11-APR-2002.

PF 03-OCT-2001; 2001WO-US31139.

PR 06-OCT-2000; 2000US-0684361.

PR 09-OCT-2000; 2000US-0685830.

PR 15-FEB-2001; 2001US-0785019.

PR 24-AUG-2001; 2001US-0938864.

PA (CORI-) CORIXA CORP.

PA (GAIG/) GAIGER A.

PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;

PI Sleath PR, Moseman S, Evans L, Spies AG, Boydston J;

DR WPI; 2002-352217/38.

XX Novel isolated WTI polynucleotide, and encoded polypeptide, useful for  
 PT treating and diagnosing cancer in a patient -

XX Example 4; Page 210; 260pp; English.

XX The invention relates to an isolated WTI polynucleotide (I) and  
 CC polypeptide encoded by (I). The WTI polynucleotides and polypeptides  
 CC are used for treating and detecting cancer in a patient, and for  
 CC stimulating an immune response in patient. ABG33070-ABG33405  
 CC represent WTI amino acid sequences of the invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 51; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9  
 Db 1 RMPFNAPYL 9

RESULT 12

AAE17298  
 ID AAE17298 standard; peptide; 9 AA.

AC AAE17298;

DT 18-APR-2002 (first entry)

DE Human leukocyte antigen (HLA-A2.1) restricted peptide, Db126.

KW Human; artificial antigen presenting cell; APC; beta2-microglobulin;  
 KW human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW cytotoxic T lymphocyte; CTL; T cell-specific antigen; TCA; antitumour;  
 KW immune response; cancer.

OS Homo sapiens.

PN WO200194944-A2.

PD 13-DEC-2001.

PF 01-JUN-2001; 2001WO-US17981.

PR 02-JUN-2000; 2000US-209157P.

PA (SLOK) SLOAN KETTERING INST CANCER RES.

PI Sadelain M, Latouche J;

DR WPI; 2002-139667/18.

PT Artificial antigen presenting cells for activating T lymphocytes,  
 PT comprises eukaryotic cell expressing antigen presenting complex having  
 PT beta2-microglobulin, exogenous accessory molecule, human leukocyte  
 PT antigen molecule and protein -

XX Example 17; Page 40; 75pp; English.

XX The present invention relates to an artificial antigen presenting cell  
 CC (APC) comprising a eukaryotic cell expressing an antigen presenting  
 CC complex comprising beta2-microglobulin, an exogenous accessory molecule,  
 CC a human leukocyte antigen, HLA (major histocompatibility complex, MHC)  
 CC molecule of a single type and a protein that is processed intracellularly  
 CC to produce an exogenous T cell-specific epitope. The invention also  
 CC relates to methods for activation of T lymphocytes. The method is also  
 CC useful for identifying within a test population of cytotoxic T  
 CC lymphocytes (CTLs), CTLs specifically activated against a known T-cell  
 CC specific antigen (TCA), which is useful for diagnostic purposes. APC is  
 CC also useful for activating CTLs, by contacting APC with a suitable  
 CC population of T lymphocytes under conditions suitable for the activation  
 CC and isolating the activated CTLs. APC is further useful for the  
 CC investigation of primary T cell activation and diagnostic applications  
 CC here primary T cell activation allow discovery of antigens and accessory  
 CC molecules, and diagnostic applications include cell-based assays for  
 CC quantifying immune response in normal, infected or treated (vaccinated)  
 CC patients. Composition comprising APC or activated T cells produced by  
 CC utilizing APC is useful for eliciting an antitumour response. The  
 CC invention is used for the treatment of cancer. The present sequence is  
 CC human HLA-A2.1 restricted peptide used in additional APC-induced CTL-  
 CC activation.

XX Sequence 9 AA;

Query Match 100.0%; Score 51; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMPFNAPYL 9

Db 1 RMFPNAPYL 9

## RESULT 13

AAV98502 ID AAV98502 standard; Peptide; 23 AA.

XX AAV98502;

XX 31-JUL-2000 (first entry)

XX Human WT1 peptide SEQ ID NO:2.

XX WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;  
XX metastatic disease; mouse; human; Wilm's tumour; immune response;  
XX vaccine.

XX Homo sapiens.

XX WO200018795-A2.

XX 06-APR-2000.

XX 30-SEP-1999; 99WO-US22819.

XX 30-SEP-1998; 98US-0164223.

XX 25-MAR-1999; 99US-0276484.

XX (CORI-) CORIXA CORP.

XX (GALG/) GALGER A.

XX Gaiger A, Cheever M;

XX WPI; 2000-293107/25.

XX Novel polypeptides comprising an immunogenic portion of a native WT1  
XX polypeptide, useful for inhibiting the development of malignant  
XX diseases associated with WT1 expression e.g. leukemia or cancer -

XX Claim 4; Page 46; 193pp; English.

XX The present invention describes polypeptides (I) comprising an  
XX immunogenic portion of a native Wilm's Tumour gene product polypeptide,  
XX WT1, (or variants of the immunogenic portion retaining the ability to  
XX react with WT1-specific antisera and/or T-cell lines or clones) and  
XX comprising 16 consecutive amino acids (aa) or less of a native WT1  
XX polypeptide. The polypeptides are useful therapeutically and to  
XX manufacture medicaments for enhancing/inducing an immune response in  
XX patients. The polypeptides, mimetics or polynucleotides can be included  
XX with a carrier/excipient in pharmaceutical compositions or with a  
XX non-specific immune response enhancer (e.g. an adjuvant or enhancer  
XX preferentially enhancing a T cell response) in vaccines. Pharmaceutical  
XX compositions and vaccines can be administered to human patients to  
XX enhance or induce an immune response specific for WT1 or a cell  
XX expressing WT1, useful to inhibit the development of malignant diseases  
XX associated with WT1 expression, e.g. leukemia (especially acute/chronic  
XX myeloid leukemia or acute lymphocytic leukemia) or cancer (especially  
XX breast, lung, thyroid or gastrointestinal cancer, or a melanoma).  
XX AAV98501 to AAV98811 represent polypeptide sequences, and AAV13848 to  
XX AAV13862 represent PCR primers, used in the exemplification of the  
XX present invention.

XX Sequence 23 AA;

XX Query Match 100.0%; Score 51; DB 21; Length 23;

XX Best Local Similarity 100.0%; Pred. No. 0.007;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9

Db 10 RMFPNAPYL 18

## RESULT 14

AAV98503 ID AAV98503 standard; Peptide; 23 AA.

XX AAV98503;

XX 31-JUL-2000 (first entry)

XX Mouse WT1 peptide SEQ ID NO:3.

XX WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;  
XX metastatic disease; mouse; human; Wilm's tumour; immune response;  
XX vaccine.

XX Mus musculus.

XX WO200018795-A2.

XX 06-APR-2000.

XX 30-SEP-1999; 99WO-US22819.

XX 30-SEP-1998; 98US-0164223.

XX 25-MAR-1999; 99US-0276484.

XX (CORI-) CORIXA CORP.

XX (GALG/) GALGER A.

XX Gaiger A, Cheever M;

XX WPI; 2000-293107/25.

XX Novel polypeptides comprising an immunogenic portion of a native WT1  
XX polypeptide, useful for inhibiting the development of malignant  
XX diseases associated with WT1 expression e.g. leukemia or cancer -

XX Example 3; Page 46; 193pp; English.

XX The present invention describes polypeptides (I) comprising an  
XX immunogenic portion of a native Wilm's Tumour gene product polypeptide,  
XX WT1, (or variants of the immunogenic portion retaining the ability to  
XX react with WT1-specific antisera and/or T-cell lines or clones) and  
XX comprising 16 consecutive amino acids (aa) or less of a native WT1  
XX polypeptide. The polypeptides are useful therapeutically and to  
XX manufacture medicaments for enhancing/inducing an immune response in  
XX patients. The polypeptides, mimetics or polynucleotides can be included  
XX with a carrier/excipient in pharmaceutical compositions or with a  
XX non-specific immune response enhancer (e.g. an adjuvant or enhancer  
XX preferentially enhancing a T cell response) in vaccines. Pharmaceutical  
XX compositions and vaccines can be administered to human patients to  
XX enhance or induce an immune response specific for WT1 or a cell  
XX expressing WT1, useful to inhibit the development of malignant diseases  
XX associated with WT1 expression, e.g. leukemia (especially acute/chronic  
XX myeloid leukemia or acute lymphocytic leukemia) or cancer (especially  
XX breast, lung, thyroid or gastrointestinal cancer, or a melanoma).  
XX AAV98501 to AAV98811 represent polypeptide sequences, and AAV13848 to  
XX AAV13862 represent PCR primers, used in the exemplification of the  
XX present invention.

XX Sequence 23 AA;

XX Query Match 100.0%; Score 51; DB 21; Length 23;

XX Best Local Similarity 100.0%; Pred. No. 0.007;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9

Db 10 RMFPNAPYL 18

## RESULT 15

AAU68601

```

ID AAU68601 standard; Peptide; 23 AA.
XX
XX AAU68601;
AC
XX 16-JAN-2002 (first entry)
DT
XX
XX Human Wilm's tumour protein, WT1, antigenic peptide #2.
DE
XX
XX Human; Wilms' tumour; WT1; pleural mesothelioma; antigen;
KW leukaemia; acute myeloid leukaemia; ALL; chronic myeloid leukaemia; CML;
KW acute lymphocytic leukaemia; ALL; myelodysplastic syndromes;
KW myeloproliferative syndrome; cancer; cytostatic.
XX
XX Homo sapiens.
OS
XX WO200162920-A2.
PN
XX 30-AUG-2001.
PD
XX 22-FEB-2001; 2001WO-US05702.
PP
XX 22-FEB-2000; 2000US-184070P.
PR
XX (CORI-) CORIXA CORP.
PA
XX Cheever MA, Galger A;
PI
XX WPI; 2001-648218/74.
DR
XX
XX Composition for the treatment of mesothelioma comprises specific
PT peptides i.e. Wilms' tumour antigen polypeptide derived antigenic
PT fragments -
XX
XX Claim 1; Page 24; 242pp; English.
PS
XX The invention relates to the use of a composition comprising at least a
CC first isolated peptide, of between 9 and 40 amino acids or a first
CC nucleic acid, encoding the peptide, in the manufacture of a medicament
CC for treating or preventing mesothelioma. The peptides are antigenic
CC peptides derived from the Wilms' tumour protein WT1. The composition is
CC useful for the treatment of mesothelioma, Wilms' tumour, preferably
CC pleural mesothelioma and other WT1 associated malignancies e.g.
CC leukaemia (including acute myeloid leukaemia, ALL, chronic myeloid
CC leukaemia, CML, acute lymphocytic leukaemia, ALL, and childhood ALL),
CC myelodysplastic syndromes, myeloproliferative syndromes and cancers
CC (e.g. breast, testicular, prostate, lung and ovarian) in mammals,
CC preferably humans. The present sequence is an antigenic peptide of
CC the invention derived from human WT1.
XX
XX Sequence 23 AA;
SQ
Query Match 100.0%; Score 51; DB 22; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RMFPNAPYL 9
DB 10 RMFPNAPYL 18

```

```

KW myeloproliferative syndrome; cancer; cytostatic.
XX
XX Mus musculus.
OS
XX WO200162920-A2.
PN
XX 30-AUG-2001.
PD
XX 22-FEB-2001; 2001WO-US05702.
PP
XX 22-FEB-2000; 2000US-184070P.
PR
XX (CORI-) CORIXA CORP.
PA
XX Cheever MA, Galger A;
PI
XX WPI; 2001-648218/74.
DR
XX
XX Composition for the treatment of mesothelioma comprises specific
PT peptides i.e. Wilms' tumour antigen polypeptide derived antigenic
PT fragments -
XX
XX Claim 1; Page 24; 242pp; English.
PS
XX The invention relates to the use of a composition comprising at least a
CC first isolated peptide, of between 9 and 40 amino acids or a first
CC nucleic acid, encoding the peptide, in the manufacture of a medicament
CC for treating or preventing mesothelioma. The peptides are antigenic
CC peptides derived from the Wilms' tumour protein WT1. The composition is
CC useful for the treatment of mesothelioma, Wilms' tumour, preferably
CC pleural mesothelioma and other WT1 associated malignancies e.g.
CC leukaemia (including acute myeloid leukaemia, ALL, chronic myeloid
CC leukaemia, CML, acute lymphocytic leukaemia, ALL, and childhood ALL),
CC myelodysplastic syndromes, myeloproliferative syndromes and cancers
CC (e.g. breast, testicular, prostate, lung and ovarian) in mammals,
CC preferably humans. The present sequence is an antigenic peptide of
CC the invention derived from mouse WT1.
XX
XX Sequence 23 AA;
SQ
Query Match 100.0%; Score 51; DB 22; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RMFPNAPYL 9
DB 10 RMFPNAPYL 18

```

```

RESULT 16
AAU68602
ID AAU68602 standard; Peptide; 23 AA.
XX
XX AAU68602;
AC
XX
XX 16-JAN-2002 (first entry)
DT
XX
XX Mouse Wilm's tumour protein, WT1, antigenic peptide #1.
DE
XX
XX Mouse; Wilms' tumour; WT1; pleural mesothelioma; antigen;
KW leukaemia; acute myeloid leukaemia; ALL; chronic myeloid leukaemia; CML;
KW acute lymphocytic leukaemia; ALL; myelodysplastic syndromes;
XX

```

```

RESULT 17
AAG61834
ID AAG61834 standard; Peptide; 23 AA.
XX
XX AAG61834;
AC
XX
XX 06-JUL-2001 (first entry)
DT
XX
XX Human WT1 immunogenic peptide SEQ ID NO: 2.
DE
XX
XX Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;
KW chromosome 11p13; zinc finger transcription factor.
KW
XX
XX Homo sapiens.
OS
XX WO200125273-A2.
PN
XX 12-APR-2001.
PD
XX 04-OCT-2000; 2000WO-US27465.
PP
XX 04-OCT-1999; 99US-0157459.
PR
XX (CORI-) CORIXA CORP.
PA

```

XX Skeiky YAW, Xu J, Cheever MA, Reed SG;  
 XX WPI; 2001-328324/34.  
 XX Polypeptide comprising part of the Wilm's Tumour gene product sequence is  
 PT used in the diagnosis and treatment of malignant diseases e.g. leukemia  
 PT and cancer associated with WT1 -  
 XX  
 XX Claim 4; Page 155; 228pp; English.  
 XX  
 CC The present invention describes compositions comprising peptides derived  
 CC from the Wilm's tumour protein WT1 and methods for their use in treating  
 CC malignant diseases. Peptides derived from both the murine and human WT1  
 CC proteins are provided. The human WT1 gene is found on chromosome 11p13,  
 CC and the protein was shown to be a zinc finger transcription factor. The  
 CC immunogenic peptides of the invention are particularly useful in the  
 CC diagnosis and treatment of cancer and leukaemia. The present sequence is  
 CC a polypeptide described in the exemplification of the invention.  
 CC  
 XX Sequence 23 AA;  
 SO  
 Query Match 100.0%; Score 51; DB 22; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 0.007;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RMFPNAPYL 9  
 DB 10 RMFPNAPYL 18  
 RESULT 18  
 AAG61835  
 ID AAG61835 standard; Peptide; 23 AA.  
 XX AAG61835;  
 AC  
 XX 06-JUL-2001 (first entry)  
 DT  
 XX Mouse WT1 immunogenic peptide SEQ ID NO: 3.  
 DE  
 XX Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;  
 KW chromosome 11p13; zinc finger transcription factor.  
 KM  
 XX Mus musculus.  
 OS  
 XX WO200125273-A2.  
 PN  
 XX 12-APR-2001.  
 PD  
 XX 04-OCT-2000; 2000WO-US27465.  
 PF  
 XX 04-OCT-1999; 99US-0157459.  
 PR  
 XX (CORI-) CORIXA CORP.  
 PA  
 XX Skeiky YAW, Xu J, Cheever MA, Reed SG;  
 PI WPI; 2001-328324/34.  
 DR  
 XX Polypeptide comprising part of the Wilm's Tumour gene product sequence is  
 PT used in the diagnosis and treatment of malignant diseases e.g. leukemia  
 PT and cancer associated with WT1 -  
 XX  
 XX Example 3; Page 155; 228pp; English.  
 XX  
 CC The present invention describes compositions comprising peptides derived  
 CC from the Wilm's tumour protein WT1 and methods for their use in treating  
 CC malignant diseases. Peptides derived from both the murine and human WT1  
 CC proteins are provided. The human WT1 gene is found on chromosome 11p13,  
 CC and the protein was shown to be a zinc finger transcription factor. The  
 CC immunogenic peptides of the invention are particularly useful in the  
 CC diagnosis and treatment of cancer and leukaemia. The present sequence is

CC a polypeptide described in the exemplification of the invention.  
 XX  
 XX Sequence 23 AA;  
 SO  
 Query Match 100.0%; Score 51; DB 22; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 0.007;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RMFPNAPYL 9  
 DB 10 RMFPNAPYL 18  
 RESULT 19  
 ABG33071  
 ID ABG33071 standard; Peptide; 23 AA.  
 XX ABG33071;  
 AC  
 XX 15-JUL-2002 (first entry)  
 DT  
 XX Human WT1 immunogenic peptide #2.  
 DE  
 XX Human; mouse; cytostatic; immunostimulant; WT1; cancer;  
 KW immune response.  
 KM  
 XX Homo sapiens.  
 OS  
 XX WO200228414-A1.  
 PN  
 XX 11-APR-2002.  
 PD  
 XX 03-OCT-2001; 2001WO-US31139.  
 PF  
 XX 06-OCT-2000; 2000US-0684361.  
 PR  
 XX 09-OCT-2000; 2000US-0685830.  
 PR  
 XX 15-FEB-2001; 2001US-0785019.  
 PR  
 XX 24-AUG-2001; 2001US-0938864.  
 XX  
 XX (CORI-) CORIXA CORP.  
 PA  
 XX (GAIg/) GAIGER A.  
 PI  
 XX Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;  
 PI Steach PR, Moseman S, Evans L, Spies AG, Boydscon J;  
 PI WPI; 2002-352217/38.  
 DR  
 XX Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for  
 PT treating and diagnosing cancer in a patient -  
 PT  
 XX Example 3; Page 165; 260pp; English.  
 PS  
 XX The invention relates to an isolated WT1 polynucleotide (1) and  
 CC polypeptide encoded by (1). The WT1 polynucleotides and polypeptides  
 CC are used for treating and detecting cancer in a patient, and for  
 CC stimulating an immune response in patient. ABG33070-ABG33405  
 CC represent WT1 amino acid sequences of the invention.  
 CC  
 XX Sequence 23 AA;  
 SO  
 Query Match 100.0%; Score 51; DB 23; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 0.007;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RMFPNAPYL 9  
 DB 10 RMFPNAPYL 18  
 RESULT 20  
 ABG33072  
 ID ABG33072 standard; Peptide; 23 AA.  
 XX

AC ABG33072;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Mouse WT1 immunogenic peptide #1.  
 XX  
 KW Human; mouse; cytostatic; immunostimulant; WT1; cancer;  
 KW immune response.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200228414-A1.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 03-OCT-2001; 2001WO-US31139.  
 XX  
 PR 06-OCT-2000; 2000US-0684361.  
 PR 09-OCT-2000; 2000US-0685830.  
 PR 15-FEB-2001; 2001US-0785019.  
 PR 24-AUG-2001; 2001US-0938864.  
 XX  
 PA (CORI-) CORIXA CORP.  
 PA (GAIG/) GAIGER A.  
 XX  
 PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;  
 PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;  
 DR WPI; 2002-352217/38.  
 XX  
 PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for  
 PT treating and diagnosing cancer in a patient -  
 XX  
 PS Example 3; Page 165; 260pp; English.  
 XX  
 CC The invention relates to an isolated WT1 polynucleotide (I) and  
 CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides  
 CC are used for treating and detecting cancer in a patient, and for  
 CC stimulating an immune response in patient. ABG33070-ABG33405  
 CC represent WT1 amino acid sequences of the invention.  
 XX  
 SQ Sequence 23 AA;  
 Query Match 100.0%; Score 51; DB 23; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 0.007;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RMFPNAPYL 9  
 DB 10 RMFPNAPYL 18  
 RESULT 21  
 ABG33387  
 ID ABG33387 standard; Protein; 152 AA.  
 XX  
 AC ABG33387;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Human WT1-T12.  
 XX  
 KW Human; mouse; cytostatic; immunostimulant; WT1; cancer;  
 KW immune response.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200228414-A1.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 03-OCT-2001; 2001WO-US31139.  
 XX

PR 06-OCT-2000; 2000US-0684361.  
 PR 09-OCT-2000; 2000US-0685830.  
 PR 15-FEB-2001; 2001US-0785019.  
 PR 24-AUG-2001; 2001US-0938864.  
 XX  
 PA (CORI-) CORIXA CORP.  
 PA (GAIG/) GAIGER A.  
 XX  
 PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;  
 PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;  
 DR WPI; 2002-352217/38.  
 DR N-PSDB; ABK69669.  
 XX  
 PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for  
 PT treating and diagnosing cancer in a patient -  
 XX  
 PS Claim 2; Page 226-227; 260pp; English.  
 XX  
 CC The invention relates to an isolated WT1 polynucleotide (I) and  
 CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides  
 CC are used for treating and detecting cancer in a patient, and for  
 CC stimulating an immune response in patient. ABG33070-ABG33405  
 CC represent WT1 amino acid sequences of the invention.  
 XX  
 SQ Sequence 152 AA;  
 Query Match 100.0%; Score 51; DB 23; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RMFPNAPYL 9  
 DB 51 RMFPNAPYL 59  
 RESULT 22  
 AAM47175  
 ID AAM47175 standard; Protein; 154 AA.  
 XX  
 AC AAM47175;  
 XX  
 DT 01-JUN-1998 (first entry)  
 XX  
 DE Wilms' tumour polypeptide (WT33) proline and glutamine rich region.  
 XX  
 KW Wilms' tumour; WT33; cancer treatment; antibody production; WAGR;  
 KW Denys-drash syndrome; WT1.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5726288-A.  
 XX  
 PD 10-MAR-1998.  
 XX  
 PF 02-AUG-1993; 93US-0102942.  
 XX  
 PR 02-AUG-1993; 93US-0102942.  
 PR 13-NOV-1989; 89US-0435780.  
 PR 13-NOV-1990; 90US-0614161.  
 XX  
 PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 XX  
 PI Bruening W, Buckler AJ, Call KM, Darveau A, Glaeser TM;  
 PI Haber DA, Housman DE, Ito CY, Pelletier J, Rose EA;  
 DR WPI; 1998-192828/17.  
 XX  
 PT New Wilms' tumour polypeptide - useful for, e.g. cancer treatment  
 PT and antibody production  
 XX  
 PS Claim 2; Fig 4; 42pp; English.  
 XX

CC This sequence represents the proline and glutamine rich region of a new  
 CC Wilms' tumour (WT33) polypeptide. The Wilms' tumour gene (WT1) is  
 CC associated with 11p3 locus on the human chromosome. This proline and  
 CC glutamine rich region indicates that the Wilms' tumour polypeptide has  
 CC a role in transcription regulation. The polypeptide or immunogenic  
 CC fragments of the polypeptide can be used to treat cancerous or  
 CC precancerous conditions (especially Wilms' tumour), or to raise  
 CC antibodies for diagnostic use. The product allow detection of risk of  
 CC development of Wilms' tumour, e.g. in diseases such as WAGR and  
 CC Denys-Drash syndrome, to be assessed prior to current methods of  
 CC detection.

CC Sequence 154 AA;

Query Match 100.0%; Score 51; DB 19; Length 154;  
 Best Local Similarity 100.0%; Pred. No. 0.055;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9  
 Db 40 RMPFNAPYL 48

# RESULT 23

ID AAG78445 standard; Protein; 154 AA.

AC AAG78445;

DT 12-APR-2002 (first entry)

DE Amino acid sequence of the proline/glutamine rich region of WT33.

KM Tumour; oncogene; retinoblastoma; chromosome 11p13; zinc finger;

KW Wilms' tumour disease; WT33; human.

OS Homo sapiens.

PN US6316599-B1.

PD 13-NOV-2001.

PF 09-MAR-1998; 98US-0037179.

PR 02-AUG-1993; 93US-0102942.

PR 13-NOV-1989; 89US-0435780.

PR 13-NOV-1990; 90US-0614161.

PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.

PI Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J, Haber DA;  
 PI Rose EA, Housman DE, Breuning W, Darveau A;

DR WPI; 2002-074379/10.

PT Antibodies specific for Wilms' tumour (WT) protein variant WT33, useful  
 PT in immunoassays to detect WT33 in samples and diagnose e.g. Sporadic  
 PT Wilms' tumours -

PS Claim 5; Fig 4; 45pp; English.

XX This invention relates to an isolated antibody specific for a protein  
 CC encoded by a Wilms' tumour DNA. The antibodies may be used in  
 CC immunoassays to detect the presence of the Wilms' tumour variant WT33 in  
 CC biological samples. They may be used in this way to diagnose sporadic  
 CC Wilms' tumours, as seen in Wilms' tumour. The antibody makes it possible  
 CC to detect proteins encoded by DNA which is clearly derived from the 11p13  
 CC Wilms' tumour gene. This is particularly valuable because the treatment  
 CC of Wilms' tumour represents one of the clearest examples of success in  
 CC paediatric oncology. As a result of the development of effective  
 CC therapeutic regimens, a diagnostic test would allow early detection of  
 CC the disease. The presence of the disease can be confirmed, thus making  
 CC it possible to intervene therapeutically prior to or at an earlier

CC stage in the development of the disease. This sequence represents  
 CC the proline/glutamine rich region of the WT33 Wilms' tumour protein,  
 CC encoded by the gene located on chromosome 11p13.

CC Sequence 154 AA;

Query Match 100.0%; Score 51; DB 23; Length 154;  
 Best Local Similarity 100.0%; Pred. No. 0.055;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9  
 Db 40 RMPFNAPYL 48

# RESULT 24

ID ABG71422 standard; Protein; 154 AA.

AC ABG71422;

DT 10-FEB-2003 (first entry)

DE Human Wilms' tumour gene WT33 polypeptide proline/glutamine rich region.

KM Human; Wilms' tumour gene; WT33; cytostatic; Wilms' tumour; leukaemia;

KW testicular cancer; ovarian cancer; proline/glutamine rich region.

OS Homo sapiens.

PN US2002128196-A1.

PD 12-SEP-2002.

PF 12-NOV-2001; 2001US-0993215.

PR 02-AUG-1993; 93US-0102942.

PR 09-MAR-1998; 98US-0037179.

PR 13-NOV-1989; 89US-0435780.

PR 13-NOV-1990; 90US-0614161.

PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.

PI Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J, Haber DA;  
 PI Rose EA, Housman DE, Breuning W, Darveau A;

DR WPI; 2003-066910/06.

PT Pharmaceutical composition for treating cancer or precancerous  
 PT condition such as Wilms' tumor, leukemia, testicular and ovarian cancer  
 PT associated with Wilms' tumour gene, and for inducing immune and antibody  
 PT responses -

PS Claim 1; Fig 4; 41pp; English.

XX The invention relates to a pharmaceutical composition comprising a  
 CC polypeptide encoded by a Wilms' tumour gene. The composition is useful  
 CC for treating cancer or precancerous conditions (such as Wilms' tumour,  
 CC leukaemia, testicular and ovarian cancer) associated with the Wilms'  
 CC tumour gene in an individual, for inducing an immune response which  
 CC results in antibody production in a mammal, and for inducing an antibody  
 CC response by administering the composition to the mammal. This sequence  
 CC represents a human Wilms' tumour gene polypeptide WT33 proline/glutamine  
 CC rich region.

XX Sequence 154 AA;

Query Match 100.0%; Score 51; DB 24; Length 154;  
 Best Local Similarity 100.0%; Pred. No. 0.055;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPFNAPYL 9  
 Db 40 RMPFNAPYL 48

```

Db          40 RMFPNAPYL 48

RESULT 25
AAR85066
ID AAR85066 standard; Protein; 210 AA.
XX
XX AAR85066;
AC
XX 02-FEB-1996 (first entry)
DT
XX WILMS' tumour antigen WT1-6F.
DE
XX WILMS' tumour; WT1-6F; monoclonal antibody; leukaemia.
KW
XX Chimeric Homo sapiens;
OS Chimeric synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..11
XX /label= Histidine_fusion_peptide
XX /note= "hexa-histidine peptide used to facilitate
XX fusion protein purification"
XX
XX Protein 12..192
XX /label= WT1
XX Peptide 193..219
XX /note= "vector-derived amino acids"
XX
XX MO9529995-A1.
XX
XX 09-NOV-1995.
XX
XX 25-APR-1995; 95WO-US05523.
XX
XX 28-APR-1994; 94US-0234783.
XX
XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX
XX Herlyn M, Morris J, Rauscher FJ, Rodeck U;
XX
XX WPI; 1995-393072/50.
XX N-PSDB; AAT02462.
XX
XX Monoclonal antibodies specific for WILMS' tumour protein antigen WT1
XX - useful for detecting, monitoring and diagnosing malignancies
XX characterised by expression of WT1 protein, e.g. Leukaemia
XX
XX Example 1; Page 37-38; 54pp; English.
XX
XX WILMS' tumor antigen WT1-6F (AAR85066) is based on amino acids
XX 1-181 of the native sequence, plus additional N- and C-terminal
XX sequences, and is encoded by synthetic DNA (AAT02462) optimized for
XX expression in E. coli. WT1-6F is used to raise monoclonal
XX antibodies specific for WT1.
XX
XX Sequence 210 AA;
SQ
Query Match 100.0%; Score 51; DB 16; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 RMFPNAPYL 9
Db 137 RMFPNAPYL 145

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DT 24-SEP-1997 (first entry)
XX
XX WILMS' tumour protein antigen WT1-6F.
DE
XX WILMS' tumour; WT1; antigen; WT1-6F; monoclonal; antibody;
XX diagnosis; mesothelioma; prostate; ovarian; cancer; leukaemia;
XX leukemia.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..11
XX /note= "histidine fusion peptide to facilitate
XX purification"
XX
XX Protein 12..192
XX /note= "amino acids 1-181 of WT1 protein"
XX Region 193..210
XX /note= "vector sequences added during cloning"
XX
XX US633142-A.
XX
XX 27-MAY-1997.
XX
XX 01-JUN-1995; 95US-0456907.
XX
XX 01-JUN-1995; 95US-0456907.
XX
XX 28-APR-1994; 94US-0234783.
XX
XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX
XX Herlyn M, Morris J, Rauscher FJ, Rodeck U;
XX
XX WPI; 1997-297358/27.
XX N-PSDB; AAT75529.
XX
XX Diagnosis of mesothelioma and monitoring of leukaemia therapy -
XX using monoclonal antibodies against WILMS' tumour 1 antigen
XX
XX Example 1; Columns 17-20; 21pp; English.
XX
XX The present sequence is the WILMS' tumour protein antigen
XX WT1-6F, which comprises amino acids 1-181 of the WILMS' tumour 1
XX antigen (WT1) protein. WT1-6F can be used to raise monoclonal
XX antibodies (MAb), e.g. H2, H7 and/or H17, which are secreted by
XX the hybridoma cell lines ATCC 11598, 11599 and 11600. The MAb can
XX or leukaemia by binding an antigen in a whole blood, serum, plasma,
XX synovial fluid or tissue sample, or monitor therapy in leukaemia
XX patients by binding an antigen in a whole blood, plasma, serum,
XX urine or bone marrow sample, indicating the presence of active
XX leukaemia cells.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 210 AA;
SQ
Query Match 100.0%; Score 51; DB 18; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 RMFPNAPYL 9
Db 137 RMFPNAPYL 145

```



```

DE Human WTI-E.
XX
XX Human; mouse; cytostatic; immunostimulant; WTI; cancer;
XX Immune response.
XX Homo sapiens.
XX WO200228414-A1.
XX
XX 11-APR-2002.
XX
XX 03-OCT-2001; 2001WO-US31139.
XX
XX 06-OCT-2000; 2000US-0684361.
XX 09-OCT-2000; 2000US-0685830.
XX 15-FEB-2001; 2001US-0785019.
XX 24-AUG-2001; 2001US-0938864.
XX
XX (CORI-) CORIXA CORP.
XX (GAI/ ) GAIGER A.
XX
XX Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
XX Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX
XX WPI; 2002-352217/38.
XX
XX N-PSDB; ABK69682.
XX
XX Novel isolated WTI polynucleotide, and encoded polypeptide, useful for
XX treating and diagnosing cancer in a patient -
XX
XX Claim 2; Page 248; 260pp; English.
XX
XX The invention relates to an isolated WTI polynucleotide (I) and
XX polypeptide encoded by (I). The WTI polynucleotides and polypeptides
XX are used for treating and detecting cancer in a patient, and for
XX stimulating an immune response in patient. ABG33070-ABG33405
XX represent WTI amino acid sequences of the invention.
XX
XX Sequence 214 AA;
SQ
Query Match 100.0%; Score 51; DB 23; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RMFPNAPYL 9
DB 59 RMFPNAPYL 67

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PR 24-AUG-2001; 2001US-0938864.
XX
XX (CORI-) CORIXA CORP.
XX (GAI/ ) GAIGER A.
XX
XX Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
XX Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX
XX WPI; 2002-352217/38.
XX
XX N-PSDB; ABK69666.
XX
XX Novel isolated WTI polynucleotide, and encoded polypeptide, useful for
XX treating and diagnosing cancer in a patient -
XX
XX Claim 2; Page 223-224; 260pp; English.
XX
XX The invention relates to an isolated WTI polynucleotide (I) and
XX polypeptide encoded by (I). The WTI polynucleotides and polypeptides
XX are used for treating and detecting cancer in a patient, and for
XX stimulating an immune response in patient. ABG33070-ABG33405
XX represent WTI amino acid sequences of the invention.
XX
XX Sequence 256 AA;
SQ
Query Match 100.0%; Score 51; DB 23; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RMFPNAPYL 9
DB 133 RMFPNAPYL 141

```

CC The invention relates to an isolated WT1 polynucleotide (I) and  
 CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides  
 CC are used for treating and detecting cancer in a patient, and for  
 CC stimulating an immune response in patient. ABG33070-ABG33405  
 CC represent WT1 amino acid sequences of the invention.

XX Sequence 344 AA;

Query Match 100.0%; Score 51; DB 23; Length 344;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9

Db 189 RMFPNAPYL 197

RESULT 30

AA12240 standard; Protein; 345 AA.

XX AA12240;

XX 25-MAR-2003 (updated)

XX 15-AUG-1991 (first entry)

XX Wilm's tumour gene prod.

XX Wilm's tumour; monoclonal antibodies.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Domain /label= proline/glutamine rich region

XX Domain /label= zinc finger domain 1

XX Domain /label= zinc finger domain 2

XX Domain /label= zinc finger domain 3

XX Domain /label= zinc finger domain 4

XX W09107509-A.

XX 30-MAY-1991.

XX 13-NOV-1990; 90WO-US06629.

XX 13-NOV-1989; 89US-0435780.

XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.

XX Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J;

XX Haber DA, Rose EA, Housman DE;

XX WPI; 1991-178117/24.

XX N-PSDB; AAQ12020.

XX Nucleotide sequence of human chromosome 11 band 13 Wilm's tumour

XX locus - used to diagnose, quantify and treat Wilm's tumours

XX Disclosure; fig 3; 67pp; English.

XX This polypeptide is encoded by the Wilm's tumour (WT) gene which

XX maps to the 11p13 locus of human chromosome 11. It contains 4

XX zinc finger binding domains and a proline/glutamine rich region.

XX and hence is thought to be involved in transcription regulation.

XX Using this WT protein and the DNA, probes and antibodies can be

XX developed for diagnosing WT. Lesions similar to WT may also

XX be detected.

XX (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 345 AA;

Query Match 100.0%; Score 51; DB 12; Length 345;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9

Db 42 RMFPNAPYL 50

RESULT 31

AAW47173 standard; Protein; 345 AA.

XX AAW47173;

XX 01-JUN-1998 (first entry)

XX Wilm's tumour polypeptide (WT33).

XX Wilm's tumour; WT33; cancer treatment; antibody production; WAGR;

XX Denys-drash syndrome; WT1.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region /note= "proline and glutamine rich region"

XX US5726288-A.

XX 10-MAR-1998.

XX 02-AUG-1993; 93US-0102942.

XX 02-AUG-1993; 93US-0102942.

XX 13-NOV-1989; 89US-0435780.

XX 13-NOV-1990; 90US-0614161.

XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.

XX Bruening W, Buckler AJ, Call KM, Darveau A, Glaser TM;

XX Haber DA, Housman DE, Ito CY, Pelletier J, Rose EA;

XX WPI; 1998-192828/17.

XX N-PSDB; AAV17060.

XX New Wilm's tumour polypeptide - useful for, e.g. cancer treatment

XX and antibody production

XX Claim 2; Fig 3; 42pp; English.

XX This is a new Wilm's tumour (WT33) polypeptide. The Wilm's tumour gene

XX (WT1) is associated with 11p13 locus on the human chromosome. This

XX polypeptide has a region rich in proline and glutamine (AAW47175)

XX indicating that it has a role in transcription regulation. The

XX polypeptide or immunogenic fragments of the polypeptide can be used to

XX treat cancerous or precancerous conditions (especially Wilm's tumour),

XX or to raise antibodies for diagnostic use. The product allow detection

XX of risk of development of Wilm's tumour, e.g. in diseases such as WAGR

XX and Denys-Drash syndrome, to be assessed prior to current methods of

XX detection.

XX Sequence 345 AA;

XX Query Match 100.0%; Score 51; DB 19; Length 345;

XX Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 RMFPNAPYL 9

XX

Db 42 RMFPNAPYL 50

RESULT 32  
ABG31643  
ID ABG31643 standard; Protein; 345 AA.

XX  
AC ABG31643;  
XX  
DT 19-NOV-2002 (first entry)  
XX  
DE Human Wilms' tumour (WT) WT33 protein.  
XX  
KW Human; Wilms' tumour; WT; cancer; precancerous condition; leukemia;  
KW testicular cancer; ovarian cancer; antitumour; cytosolic; gene therapy;  
XX WT33.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 3..156  
FT /note= "Proline/glutamine rich region. Specifically  
FT claimed in claim 5"  
FT Region 224..334  
FT /note= "zinc finger consensus sequence"

US2002082394-A1.  
27-JUN-2002.  
14-AUG-2001; 2001US-0929315.  
02-AUG-1993; 93US-0102942.  
PR 09-MAR-1998; 98US-0037179.  
PR 13-NOV-1989; 89US-0435780.  
PR 13-NOV-1990; 90US-0614161.  
XX  
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
XX  
PI Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J, Haber DA;  
PI Rose EA, Housman DE, Breuning W, Darveau A;  
XX  
DR WPI: 2002-690126/74.  
DR N-PSDB; AHS53729.  
XX  
PT Treating cancer or precancerous condition associated with the Wilms' tumour gene in individual, by administering polypeptide or polypeptide encoded by Wilms' tumour DNA -  
XX  
PS Claim 3; Fig 3; 41pp; English.  
XX  
CC The present invention relates to a new method of treating cancer or precancerous condition associated with the Wilms' tumour gene. The method of the invention is useful for treating a cancer or precancerous condition associated with the Wilms' tumour gene in an individual, where the cancer or precancerous condition is Wilms' tumour, leukemia, testicular cancer or ovarian cancer. The present amino acid sequence represents the human Wilms' tumour (WT) WT33 protein of the invention.  
XX  
SQ Sequence 345 AA;

Query Match 100.0%; Score 51; DB 23; Length 345;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
|||  
42 RMFPNAPYL 50

RESULT 33  
AAG78443  
ID AAG78443 standard; Protein; 345 AA.

XX  
AC AAG78443;  
XX  
DT 12-APR-2002 (first entry)  
XX  
DE WT33 Wilms' tumour protein.  
XX  
KW Tumour; oncogene; retinoblastoma; chromosome 11p13; zinc finger;  
KW Wilms' tumour disease; WT33; human.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 3..156  
FT /note= "proline/glutamine rich region"  
FT Region 224..334  
FT /note= "region in which the four zinc fingers fit  
FT the consensus sequence (see AAG78449)"

US6316599-B1.  
13-NOV-2001.  
09-MAR-1998; 98US-0037179.  
02-AUG-1993; 93US-0102942.  
PR 13-NOV-1989; 89US-0435780.  
PR 13-NOV-1990; 90US-0614161.  
XX  
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
XX  
PI Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J, Haber DA;  
PI Rose EA, Housman DE, Breuning W, Darveau A;  
XX  
DR WPI: 2002-074379/10.  
DR N-PSDB; AAH99945.  
XX  
PT Antibodies specific for Wilms' tumour (WT) protein variant WT33, useful in immunoassays to detect WT33 in samples and diagnose e.g. Sporadic Wilms' tumours -  
XX  
PS Claim 2; Fig 3; 45pp; English.  
XX  
CC This invention relates to an isolated antibody specific for a protein encoded by a Wilms' tumour DNA. The antibodies may be used in immunoassays to detect the presence of the Wilms' tumour variant WT33 in biological samples. They may be used in this way to diagnose sporadic Wilms' tumours, as seen in Wilms' tumour. The antibody makes it possible to detect proteins encoded by DNA which is clearly derived from the 11p13 Wilms' tumour gene. This is particularly valuable because the treatment of Wilms' tumour represents one of the clearest examples of success in pediatric oncology, as a result of the development of effective therapeutic regimens. A diagnostic test would allow early detection of the disease. The presence of the disease can be confirmed, thus making it possible to intervene therapeutically prior to or at an earlier stage in the development of the disease. This sequence represents the WT33 Wilms' tumour protein, encoded by the gene located on chromosome 11p13.  
XX  
SQ Sequence 345 AA;

Query Match 100.0%; Score 51; DB 23; Length 345;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
|||  
42 RMFPNAPYL 50

RESULT 34  
ABG71420  
ID ABG71420 standard; Protein; 345 AA.

```

XX AC ABG71420;
XX DT 10-FEB-2003 (first entry)
XX DE Human WILMS' tumour gene WT33 polypeptide.
XX KM Human; WILMS' tumour gene; WT33; cytostatic; WILMS' tumour; leukaemia;
XX KM testicular cancer; ovarian cancer.
XX OS Homo sapiens.
XX PN US2002128196-A1.
XX PD 12-SEP-2002.
XX PF 12-NOV-2001; 2001US-0993215.
XX PR 02-AUG-1993; 93US-0102942.
XX PR 09-MAR-1998; 98US-0037179.
XX PR 13-NOV-1989; 89US-0435780.
XX PR 13-NOV-1990; 90US-0614161.
XX PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX PI Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J, Haber DA;
XX PI Rose EA, Housman DE, Brunning W, Darveau A;
XX DR WPI; 2003-066910/06.
XX DR N-PSDB; ABS57419.
XX PT Pharmaceutical composition for treating cancer or precancerous
XX PT condition such as WILMS' tumor, leukemia, testicular and ovarian cancer
XX PT associated with WILMS' tumor gene, and for inducing immune and antibody
XX PT responses -
XX PS Example 1; Fig 3; 41pp; English.
XX CC The invention relates to a pharmaceutical composition comprising a
XX CC polypeptide encoded by a WILMS' tumor gene. The composition is useful
XX CC for treating cancer or precancerous conditions (such as WILMS' tumor,
XX CC leukaemia, testicular and ovarian cancer) associated with the WILMS'
XX CC tumor gene in an individual, for inducing an immune response which
XX CC results in antibody production in a mammal, and for inducing an antibody
XX CC response by administering the composition to the mammal. This sequence
XX CC represents a human WILMS' tumor gene polypeptide, WT33.
XX CC
XX SQ Sequence 345 AA;
XX
XX Query Match 100.0%; Score 51; DB 24; Length 345;
XX Best Local Similarity 100.0%; Pred. No. 0.13; 0; Indels 0; Gaps 0;
XX Matches 9; Conservative 0; Mismatches 0;
XX
Oy 1 RMFPNAPYL 9
Db 42 RMFPNAPYL 50
XX
RESULT 35
ABG33394
ID ABG33394 standard; Protein; 362 AA.
XX
XX ABG33394;
XX
XX 15-JUL-2002 (first entry)
XX DE Human WT1-C.
XX
XX Human; mouse; cytostatic; immunostimulant; WT1; cancer;
XX KW immune response.
XX OS Homo sapiens.
XX

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PN WO200228414-A1.
XX
XX PD 11-APR-2002.
XX
XX PF 03-OCT-2001; 2001WO-US31139.
XX
XX PR 06-OCT-2000; 2000US-0684361.
XX PR 09-OCT-2000; 2000US-0685830.
XX PR 15-FEB-2001; 2001US-0785019.
XX PR 24-AUG-2001; 2001US-0938864.
XX
XX PA (CORI-) CORIXA CORP.
XX PA (GAIG/) GAIGER A.
XX
XX PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
XX PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX
XX DR WPI; 2002-352217/38.
XX DR N-PSDB; ABK69683.
XX
XX PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
XX PT treating and diagnosing cancer in a patient -
XX PS Claim 2; Page 246-248; 260pp; English.
XX
XX CC The invention relates to an isolated WT1 polynucleotide (I) and
XX CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides
XX CC are used for treating and detecting cancer in a patient, and for
XX CC stimulating an immune response in patient. ABG33070-ABG33405
XX CC represent WT1 amino acid sequences of the invention.
XX
XX SQ Sequence 362 AA;
XX
XX Query Match 100.0%; Score 51; DB 23; Length 362;
XX Best Local Similarity 100.0%; Pred. No. 0.14; 0; Indels 0; Gaps 0;
XX Matches 9; Conservative 0; Mismatches 0;
XX
Oy 1 RMFPNAPYL 9
Db 59 RMFPNAPYL 67
XX
RESULT 36
ABG33390
ID ABG33390 standard; Protein; 369 AA.
XX
XX AC ABG33390;
XX
XX DT 15-JUL-2002 (first entry)
XX DE Human WT1-C.
XX
XX Human; mouse; cytostatic; immunostimulant; WT1; cancer;
XX KW immune response.
XX OS Homo sapiens.
XX
XX WO200228414-A1.
XX
XX 11-APR-2002.
XX
XX 03-OCT-2001; 2001WO-US31139.
XX
XX PR 06-OCT-2000; 2000US-0684361.
XX PR 09-OCT-2000; 2000US-0685830.
XX PR 15-FEB-2001; 2001US-0785019.
XX PR 24-AUG-2001; 2001US-0938864.
XX
XX PA (CORI-) CORIXA CORP.
XX PA (GAIG/) GAIGER A.
XX
XX PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
XX PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX

```

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XX  WPI: 2002-352217/38.
DR  N-PSDB; ABK69672.
XX
XX  Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
XX  treating and diagnosing cancer in a patient -
XX
XX  Claim 2; Page 228; 260pp; English.
XX
XX  The invention relates to an isolated WT1 polynucleotide (I) and
XX  polypeptide encoded by (I). The WT1 polynucleotides and polypeptides
XX  are used for treating and detecting cancer in a patient, and for
XX  stimulating an immune response in patient. ABG33070-ABG33405
XX  represent WT1 amino acid sequences of the invention.
XX
XX  Sequence 369 AA;
SQ
XX
XX  Query Match          100.0%; Score 51; DB 23; Length 369;
XX  Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
XX  Matches 9; Conservative 0;
XX
XX  1 RMFPNAPYL 9
XX  |||||
XX  66 RMFPNAPYL 74
XX
XX  RESULT 37
XX  ABG33382
XX  ID  ABG33382 standard; Protein; 410 AA.
XX
XX  AC  ABG33382;
XX
XX  DT  15-JUL-2002 (first entry)
XX
XX  DE  Human Trx_WT1_A.
XX
XX  KW  Human; mouse; cytosstatic; immunostimulant; WT1; cancer;
XX  immune response.
XX
XX  OS  Homo sapiens.
XX
XX  PN  WO200228414-A1.
XX
XX  PD  11-APR-2002.
XX
XX  PF  03-OCT-2001; 2001WO-US31139.
XX
XX  PR  06-OCT-2000; 2000US-0684361.
XX  09-OCT-2000; 2000US-0685830.
XX  15-FEB-2001; 2001US-0785019.
XX  24-AUG-2001; 2001US-0938864.
XX
XX  PA  (CORI-) CORIXA CORP.
XX  (GAIG/) GAIGER A.
XX
XX  PI  Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedrick TS;
XX  Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX
XX  DR  WPI; 2002-352217/38.
XX  N-PSDB; ABK69664.
XX
XX  PT  Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
XX  treating and diagnosing cancer in a patient -
XX
XX  PS  Claim 2; Page 221-222; 260pp; English.
XX
XX  The invention relates to an isolated WT1 polynucleotide (I) and
XX  polypeptide encoded by (I). The WT1 polynucleotides and polypeptides
XX  are used for treating and detecting cancer in a patient, and for
XX  stimulating an immune response in patient. ABG33070-ABG33405
XX  represent WT1 amino acid sequences of the invention.
XX
XX  Sequence 410 AA;
SQ

```

```

XX  Query Match          100.0%; Score 51; DB 23; Length 410;
XX  Best Local Similarity 100.0%; Pred. No. 0.16; Mismatches 0; Indels 0; Gaps 0;
XX  Matches 9; Conservative 0;
XX
XX  1 RMFPNAPYL 9
XX  |||||
XX  287 RMFPNAPYL 295
XX
XX  RESULT 38
XX  ABG33393
XX  ID  ABG33393 standard; Protein; 420 AA.
XX
XX  AC  ABG33393;
XX
XX  DT  15-JUL-2002 (first entry)
XX
XX  DE  Human Ra12/WT1-F.
XX
XX  KW  Human; mouse; cytosstatic; immunostimulant; WT1; cancer;
XX  immune response.
XX
XX  OS  Homo sapiens.
XX
XX  PN  WO200228414-A1.
XX
XX  PD  11-APR-2002.
XX
XX  PF  03-OCT-2001; 2001WO-US31139.
XX
XX  PR  06-OCT-2000; 2000US-0684361.
XX  09-OCT-2000; 2000US-0685830.
XX  15-FEB-2001; 2001US-0785019.
XX  24-AUG-2001; 2001US-0938864.
XX
XX  PA  (CORI-) CORIXA CORP.
XX  (GAIG/) GAIGER A.
XX
XX  PI  Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedrick TS;
XX  Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX
XX  DR  WPI; 2002-352217/38.
XX  N-PSDB; ABK69685.
XX
XX  PT  Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
XX  treating and diagnosing cancer in a patient -
XX
XX  PS  Claim 2; Page 245-246; 260pp; English.
XX
XX  The invention relates to an isolated WT1 polynucleotide (I) and
XX  polypeptide encoded by (I). The WT1 polynucleotides and polypeptides
XX  are used for treating and detecting cancer in a patient, and for
XX  stimulating an immune response in patient. ABG33070-ABG33405
XX  represent WT1 amino acid sequences of the invention.
XX
XX  Sequence 420 AA;
SQ
XX
XX  Query Match          100.0%; Score 51; DB 23; Length 420;
XX  Best Local Similarity 100.0%; Pred. No. 0.16; Mismatches 0; Indels 0; Gaps 0;
XX  Matches 9; Conservative 0;
XX
XX  1 RMFPNAPYL 9
XX  |||||
XX  265 RMFPNAPYL 273
XX
XX  RESULT 39
XX  ABG33397
XX  ID  ABG33397 standard; Protein; 428 AA.
XX
XX  AC  ABG33397;
XX

```

DT 15-JUL-2002 (first entry)  
 XX Human WT1 variant #1.  
 DE Human WT1 variant #1.  
 XX Human; mouse; cytostatic; immunostimulant; WT1; cancer;  
 KW immune response.  
 XX Homo sapiens.  
 OS  
 PN WO200228414-A1.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 03-OCT-2001; 2001WO-US31139.  
 XX  
 PR 06-OCT-2000; 2000US-0684361.  
 XX 09-OCT-2000; 2000US-0685830.  
 PR 15-FEB-2001; 2001US-0785019.  
 PR 24-AUG-2001; 2001US-0938864.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX (GAIG/) GAIGER A.  
 PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;  
 PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;  
 DR N-PSDB; ABK69673.  
 DR WPI; 2002-352217/38.  
 XX  
 PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for  
 PT treating and diagnosing cancer in a patient -  
 PS Claim 2; Page 251-252; 260pp; English.  
 XX  
 CC The invention relates to an isolated WT1 polynucleotide (I) and  
 CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides  
 CC are used for treating and detecting cancer in a patient, and for  
 CC stimulating an immune response in patient. ABG33070-ABG33405  
 CC represent WT1 amino acid sequences of the invention.  
 XX  
 SQ Sequence 428 AA;  
 SO

Query Match 100.0%; Score 51; DB 23; Length 428;  
 Best Local Similarity 100.0%; Pred. No. 0.17; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 |||||  
 126 RMFPNAPYL 134

Db

RESULT 40  
 AAR85065  
 ID AAR85065 standard; Protein; 429 AA.  
 XX  
 AC AAR85065;  
 XX  
 DT 02-FEB-1996 (first entry)  
 XX  
 DE WILMS' tumour WT1 antigen.  
 XX  
 KW WILMS' tumour; WT1; monoclonal antibody; leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9529995-A1.  
 XX  
 PD 09-NOV-1995.  
 XX  
 PF 25-APR-1995; 95WO-US05523.  
 XX  
 PR 28-APR-1994; 94US-0234783.  
 XX

PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.  
 XX  
 XX Herlyn M, Morris J, Rauscher FJ, Rodeck U;  
 PI WPI; 1995-393072/50.  
 DR N-PSDB; AAR85065.  
 DR  
 XX  
 PT Monoclonal antibodies specific for WILMS' tumour protein antigen WT1  
 PT - useful for detecting, monitoring and diagnosing malignancies  
 PT characterised by expression of WT1 protein, e.g. leukaemia  
 XX  
 PS Claim 1; Page 42-43; 54pp; English.  
 XX  
 CC The human WILMS' tumour antigen WT1 (sequence given in AAR85065) was  
 CC used as the basis for the design of a synthetic WT1 sequence (see  
 CC AAR85066) used to raise monoclonal antibodies specific for the antigen.  
 XX  
 SQ Sequence 429 AA;  
 SO

Query Match 100.0%; Score 51; DB 16; Length 429;  
 Best Local Similarity 100.0%; Pred. No. 0.17; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 |||||  
 126 RMFPNAPYL 134

Db

RESULT 41  
 ABG33400  
 ID ABG33400 standard; Protein; 429 AA.  
 XX  
 AC ABG33400;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Human WT1 protein, splice variant.  
 XX  
 KW Human; mouse; cytostatic; immunostimulant; WT1; cancer;  
 KW immune response.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200228414-A1.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 03-OCT-2001; 2001WO-US31139.  
 XX  
 PR 06-OCT-2000; 2000US-0684361.  
 XX 09-OCT-2000; 2000US-0685830.  
 PR 15-FEB-2001; 2001US-0785019.  
 PR 24-AUG-2001; 2001US-0938864.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX (GAIG/) GAIGER A.  
 PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;  
 PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;  
 DR N-PSDB; ABK69677.  
 DR WPI; 2002-352217/38.  
 XX  
 PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for  
 PT treating and diagnosing cancer in a patient -  
 PS Claim 2; Page 255; 260pp; English.  
 XX  
 CC The invention relates to an isolated WT1 polynucleotide (I) and  
 CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides  
 CC are used for treating and detecting cancer in a patient, and for  
 CC stimulating an immune response in patient. ABG33070-ABG33405  
 CC represent WT1 amino acid sequences of the invention.

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XX SQ Sequence 429 AA;
Query Match 100.0%; Score 51; DB 23; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RMPFNAPYL 9
   |||||
Db 126 RMPFNAPYL 134

RESULT 42
AAW47176 standard; Protein: 449 AA.
XX ID AAW47176;
XX AC AAW47176;
XX DT 01-JUN-1998 (first entry)
XX DE WILMS' tumour polypeptide (WT1).
XX KW WILMS' tumour; WT3; cancer treatment; antibody production; WAGR;
XX KM Denys-draash syndrome; WT1.
XX OS Homo sapiens.
XX PN US5726288-A.
XX PD 10-MAR-1998.
XX PF 02-AUG-1993; 93US-0102942.
XX PR 02-AUG-1993; 93US-0102942.
XX PR 13-NOV-1989; 89US-0435780.
XX PR 13-NOV-1990; 90US-0614161.
XX RA (MAST) MASSACHUSETTS INST TECHNOLOGY.
XX PI Bruening W, Buckler AJ, Call KM, Darveau A, Glaser TM;
XX PI Haber DA, Housman DE, Ito CY, Pelletier J, Rose EA;
XX DR WPI; 1998-192828/17.
XX PT New WILMS' tumour polypeptide - useful for, e.g. cancer treatment
XX PT and antibody production
XX PS Disclosure; Columns 39-42; 42pp; English.
XX CC This is a WILMS' tumour (WT1) polypeptide. The WILMS' tumour gene
XX CC (WT1) is associated with 11p3 locus on the human chromosome. The
XX CC polypeptide or immunogenic fragments of the polypeptide can be used to
XX CC treat cancerous or precancerous conditions (especially WILMS' tumour), or
XX CC to raise antibodies for diagnostic use. The product allow detection of
XX CC risk of development of WILMS' tumour, e.g. in diseases such as WAGR and
XX CC Denys-Draash syndrome, to be assessed prior to current methods of
XX CC detection.
XX SQ Sequence 449 AA;
Query Match 100.0%; Score 51; DB 19; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RMPFNAPYL 9
   |||||
Db 126 RMPFNAPYL 134

RESULT 43
AAV98804 standard; Protein: 449 AA.
XX ID AAV98804

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AC AAV98804;
XX DT 31-JUL-2000 (first entry)
XX DE Human WT1 protein sequence SEQ ID NO:319.
XX KW WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;
XX KM metastatic disease; mouse; human; WILMS' tumour; immune response;
XX KM vaccine.
XX OS Homo sapiens.
XX PN WO200018795-A2.
XX PD 06-APR-2000.
XX PF 30-SEP-1999; 99WO-US22819.
XX PR 30-SEP-1998; 98US-0164223.
XX PR 25-MAR-1999; 99US-0276484.
XX RA (CORI-) CORIYA CORP.
XX PA (GAIG/) GAIGER A.
XX PI Gaiger A, Cheever M;
XX DR WPI; 2000-293107/25.
XX PT Novel polypeptides comprising an immunogenic portion of a native WT1
XX PT polypeptide, useful for inhibiting the development of malignant
XX PT diseases associated with WT1 expression e.g. leukemia or cancer -
XX PS Disclosure; Page 190-191; 193pp; English.
XX CC The present invention describes polypeptides (I) comprising an
XX CC immunogenic portion of a native WILMS' Tumour gene product polypeptide,
XX CC WT1, (or variants of the immunogenic portion retaining the ability to
XX CC react with WT1-specific antisera and/or T-cell lines or clones) and
XX CC comprising 16 consecutive amino acids (aa) or less of a native WT1
XX CC polypeptide. The polypeptides are useful therapeutically and to
XX CC manufacture medicaments for enhancing/inducing an immune response in
XX CC patients. The polypeptides, mimetics or polynucleotides can be included
XX CC with a carrier/excipient in pharmaceutical compositions or with a
XX CC non-specific immune response enhancer (e.g. an adjuvant or enhancer
XX CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical
XX CC compositions and vaccines can be administered to human patients to
XX CC enhance or induce an immune response specific for WT1 or a cell
XX CC expressing WT1, useful to inhibit the development of malignant diseases
XX CC associated with WT1 expression, e.g. leukemia (especially acute/chronic
XX CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
XX CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma).
XX CC AAV98801 to AAV98811 represent polypeptide sequences, and AAV13848 to
XX CC AAV13862 represent PCR primers, used in the exemplification of the
XX CC present invention.
XX SQ Sequence 449 AA;
Query Match 100.0%; Score 51; DB 21; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RMPFNAPYL 9
   |||||
Db 126 RMPFNAPYL 134

RESULT 44
AAV98805 standard; Protein: 449 AA.
XX ID AAV98805
XX AC AAV98805;
XX DT 31-JUL-2000 (first entry)

```

Query Match	Best Local Similarity	Score 51;	DB 21;	Length 449;
Matches	9; Conservative	100.0%;	100.0%;	100.0%;
		0;	Mismatches	0; Indels
				Gaps
QY	1 RMFPNAPYL 9			
DB	126 RMFPNAPYL 134			
RESULT 45				
ID	AAV80196			
AC	AAV80196;			
XX				
DT	24-MAY-2000			
XX	(first entry)			
DE	Mouse Wilms' tumour suppressor gene WT1 product SEQ ID NO:1.			

KM	Wilm's tumour suppressor gene; WT1; cancer; antigen; vaccine; MHC;
XV	major histocompatibility complex; leukemia; tumour; antitumour.
XX	
OS	Mus sp.
XX	
PN	WO200006602-A1.
XX	
PD	10-FEB-2000.
XX	
PF	30-JUL-1999; 99WO-JP04130.
XX	
PR	31-JUL-1998; 98JP-0218093.
XX	
PA	(SUGI/) SUGIYAMA H.
XX	
PI	Sugiyama H, Oka Y;
XX	
DR	WPI; 2000-195264/17.
XX	
PT	Cancer antigens based on Wilm's tumor suppressor gene WT1 product or
PT	peptide derivatives; for cancer vaccines in treating leukemia and solid
PT	tumors e.g. stomach cancer, skin cancer, lung cancer and breast cancer
XX	
PS	Claim 2; Page 38-40; 48pp; Japanese.
XX	
CC	The present invention describes a cancer antigen containing the active
CC	component of Wilm's tumour suppressor gene WT1 product, or partial
CC	peptides, for cancer vaccines in treating leukaemia and solid tumours.
CC	The cancer antigens are useful for cancer vaccines in treating
CC	leukemia, bone-marrow abnormal formation syndrome, malignant lymphoma,
CC	multiple myeloma, stomach cancer, cancer of the large intestine, lung
CC	cancer, breast cancer, blastoma, liver cancer, skin cancer, bladder
CC	cancer, prostate cancer, uterus cancer, cervical cancer, or ovary
CC	cancer. The present sequence represents the mouse Wilm's tumour
CC	suppressor gene WT1 product.
XX	
SO	Sequence 449 AA;
XX	
QY	1 RMPNPAPYL 9
DG	
DB	126 RMFPNAPYL 134
XX	
RESULT 46	
ID	AAY80197 standard; protein; 449 AA.
AC	AAY80197;
DT	24-MAY-2000 (first entry)
DE	Human Wilms' tumour suppressor gene WT1 product SEQ ID NO:2.
KW	Wilm's tumour suppressor gene; WT1; cancer; antigen; vaccine; MHC;
KX	major histocompatibility complex; leukemia; tumour; antitumour.
OS	Homo sapiens.
XX	
PN	WO200006602-A1.
XX	
PD	10-FEB-2000.
XX	
PF	30-JUL-1999; 99WO-JP04130.
XX	
PR	31-JUL-1998; 98JP-0218093.
XX	
PA	(SUGI/) SUGIYAMA H.
XX	
PI	Sugiyama H, Oka Y;



XX WPI; 2000-195264/17.  
 DR  
 XX Cancer antigens based on Wilm's tumor suppressor gene WT1 product or  
 PT peptide derivatives, for cancer vaccines in treating leukemia and solid  
 PT tumors e.g. stomach cancer, skin cancer, lung cancer and breast cancer  
 XX  
 PS Claim 2; Page 40-42; 48pp; Japanese.  
 CC The present invention describes a cancer antigen containing the active  
 CC component of Wilm's tumor suppressor gene WT1 product, or partial  
 CC peptides, for cancer vaccines in treating leukemia and solid tumours.  
 CC The cancer antigens are useful for cancer vaccines in treating  
 CC leukemia, bone-marrow abnormal formation syndrome, malignant lymphoma,  
 CC multiple myeloma, stomach cancer, cancer of the large intestine, lung  
 CC cancer, breast cancer, blastoma, liver cancer, skin cancer, bladder  
 CC cancer, prostate cancer, uterus cancer, cervical cancer, or ovary  
 CC cancer. The present sequence represents the human Wilm's tumor  
 CC suppressor gene WT1 product.  
 CC  
 SQ Sequence 449 AA;  
 Query Match 100.0%; Score 51; DB 21; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RMFPNAPYL 9  
 |||||  
 Db 126 RMFPNAPYL 134  
 RESULT 47  
 AAU68903  
 ID AAU68903 standard; Protein; 449 AA.  
 AC AAU68903;  
 XX  
 DT 16-JAN-2002 (first entry)  
 XX  
 DE Human Wilm's tumour protein, WT1.  
 XX  
 XX Human; Wilm's tumour; WT1; pleural mesothelioma; antigen;  
 KW leukemia; acute myeloid leukemia; ALL; chronic myeloid leukemia; CML;  
 KW acute lymphocytic leukemia; ALL; myelodysplastic syndromes;  
 KW myeloproliferative syndrome; cancer; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200162920-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 22-FEB-2001; 2001WO-US05702.  
 XX  
 PR 22-FEB-2000; 2000US-184070P.  
 XX  
 PA (CORI-) CORIXA CORP.  
 PI Cheever MA, Gaiger A;  
 XX  
 DR WPI; 2001-648218/74.  
 XX  
 PT Composition for the treatment of mesothelioma comprises specific  
 PT peptides i.e. Wilm's tumour antigen polypeptide derived antigenic  
 PT fragments -  
 XX  
 PS Disclosure; Page 250-251; 242pp; English.  
 CC The invention relates to the use of a composition comprising at least a  
 CC first isolated peptide, of between 9 and 40 amino acids or a first  
 CC nucleic acid, encoding the peptide, in the manufacture of a medicament  
 CC for treating or preventing mesothelioma. The peptides are antigenic  
 CC peptides derived from the Wilm's tumour protein WT1. The composition is

CC useful for the treatment of mesothelioma, Wilm's tumour, preferably  
 CC pleural mesothelioma and other WT1 associated malignancies e.g.  
 CC leukemia (including acute myeloid leukemia, ALL, and childhood ALL),  
 CC leukemia, CML, acute lymphocytic leukemia, ALL, and childhood ALL),  
 CC myelodysplastic syndromes, myeloproliferative syndromes and cancers  
 CC (e.g. breast, testicular, prostate, lung and ovarian) in mammals,  
 CC preferably humans. The present sequence is the WT1 protein from which the  
 CC antigenic peptides of the invention are derived.  
 CC  
 SQ Sequence 449 AA;  
 Query Match 100.0%; Score 51; DB 22; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RMFPNAPYL 9  
 |||||  
 Db 126 RMFPNAPYL 134  
 RESULT 48  
 AAU68904  
 ID AAU68904 standard; Protein; 449 AA.  
 AC AAU68904;  
 XX  
 DT 16-JAN-2002 (first entry)  
 XX  
 DE Mouse Wilm's tumour protein, WT1.  
 XX  
 XX Mouse; Wilm's tumour; WT1; pleural mesothelioma; antigen;  
 KW leukemia; acute myeloid leukemia; ALL; chronic myeloid leukemia; CML;  
 KW acute lymphocytic leukemia; ALL; myelodysplastic syndromes;  
 KW myeloproliferative syndrome; cancer; cytostatic.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200162920-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 22-FEB-2001; 2001WO-US05702.  
 XX  
 PR 22-FEB-2000; 2000US-184070P.  
 XX  
 PA (CORI-) CORIXA CORP.  
 PI Cheever MA, Gaiger A;  
 XX  
 DR WPI; 2001-648218/74.  
 XX  
 PT Composition for the treatment of mesothelioma comprises specific  
 PT peptides i.e. Wilm's tumour antigen polypeptide derived antigenic  
 PT fragments -  
 XX  
 PS Disclosure; Page 251-252; 242pp; English.  
 CC The invention relates to the use of a composition comprising at least a  
 CC first isolated peptide, of between 9 and 40 amino acids or a first  
 CC nucleic acid, encoding the peptide, in the manufacture of a medicament  
 CC for treating or preventing mesothelioma. The peptides are antigenic  
 CC peptides derived from the Wilm's tumour protein WT1. The composition is  
 CC useful for the treatment of mesothelioma, Wilm's tumour, preferably  
 CC pleural mesothelioma and other WT1 associated malignancies e.g.  
 CC leukemia (including acute myeloid leukemia, ALL, and childhood ALL),  
 CC leukemia, CML, acute lymphocytic leukemia, ALL, and childhood ALL),  
 CC myelodysplastic syndromes, myeloproliferative syndromes and cancers  
 CC (e.g. breast, testicular, prostate, lung and ovarian) in mammals,  
 CC preferably humans. The present sequence is the WT1 protein from which the  
 CC antigenic peptides of the invention are derived.  
 CC  
 SQ Sequence 449 AA;

Query Match 100.0%; Score 51; DB 22; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 |||||  
 Db 126 RMFPNAPYL 134

RESULT 49

AAG62136

ID AAG62136 standard; Protein; 449 AA.

XX AAG62136;

XX 06-JUL-2001 (first entry)

XX Human WT1 protein SEQ ID NO: 319.

XX Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;

XX chromosome 11p13; zinc finger transcription factor.

XX Homo sapiens.

XX WO200125273-A2.

XX 12-APR-2001.

XX 04-OCT-2000; 2000WO-US27465.

XX PR 04-OCT-1999; 99US-0157459.

XX (CORI-) CORIXA CORP.

XX Skeiky YAW, Xu J, Cheever MA, Reed SG;

XX WPI; 2001-328324/34.

XX Polypeptide comprising part of the Wilm's Tumour gene product sequence is  
 PT used in the diagnosis and treatment of malignant diseases e.g. leukemia  
 PT and cancer associated with WT1 -

XX Disclousure; Page 204-205; 228pp; English.

XX The present invention describes compositions comprising peptides derived  
 CC from the Wilm's tumour protein WT1 and methods for their use in treating  
 CC malignant diseases. Peptides derived from both the murine and human WT1  
 CC proteins are provided. The human WT1 gene is found on chromosome 11p13,  
 CC and the protein was shown to be a zinc finger transcription factor. The  
 CC immunogenic peptides of the invention are particularly useful in the  
 CC diagnosis and treatment of cancer and leukaemia. The present sequence is  
 CC a polypeptide described in the exemplification of the invention.

SQ Sequence 449 AA;

Query Match 100.0%; Score 51; DB 22; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 |||||  
 Db 126 RMFPNAPYL 134

RESULT 50

AAG62137

ID AAG62137 standard; Protein; 449 AA.

XX AAG62137;

XX 06-JUL-2001 (first entry)

XX Mouse WT1 protein SEQ ID NO: 320.

XX Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;  
 KW chromosome 11p13; zinc finger transcription factor.

XX Mus musculus.

XX WO200125273-A2.

XX 12-APR-2001.

XX 04-OCT-2000; 2000WO-US27465.

XX PR 04-OCT-1999; 99US-0157459.

XX (CORI-) CORIXA CORP.

XX Skeiky YAW, Xu J, Cheever MA, Reed SG;

XX WPI; 2001-328324/34.

XX Polypeptide comprising part of the Wilm's Tumour gene product sequence is  
 PT used in the diagnosis and treatment of malignant diseases e.g. leukemia  
 PT and cancer associated with WT1 -

XX Disclousure; Page 205-206; 228pp; English.

XX The present invention describes compositions comprising peptides derived  
 CC from the Wilm's tumour protein WT1 and methods for their use in treating  
 CC malignant diseases. Peptides derived from both the murine and human WT1  
 CC proteins are provided. The human WT1 gene is found on chromosome 11p13,  
 CC and the protein was shown to be a zinc finger transcription factor. The  
 CC immunogenic peptides of the invention are particularly useful in the  
 CC diagnosis and treatment of cancer and leukaemia. The present sequence is  
 CC a polypeptide described in the exemplification of the invention.

SQ Sequence 449 AA;

Query Match 100.0%; Score 51; DB 22; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 |||||  
 Db 126 RMFPNAPYL 134

RESULT 51

ABG31644

ID ABG31644 standard; Protein; 449 AA.

XX ABG31644;

XX 19-NOV-2002 (first entry)

XX Mouse Wilm's tumour (WT) WT1 protein.

XX Mouse; Wilm's tumour; WT; cancer; precancerous condition; leukaemia;

XX testicular cancer; ovarian cancer; antitumour; cytostatic; gene therapy;

XX WT1.

XX Mus sp.

XX Key

XX Region

XX Domain

XX US2002082394-A1.

XX 27-JUN-2002.

XX 14-AUG-2001; 2001US-0929315.

Location/Qualifiers  
 250..266  
 /note= "Alternatively spliced product"  
 317..438  
 /note= "Zinc finger domains"

```

XX 02-AUG-1993; 93US-0102942.
PR 09-MAR-1998; 98US-0037179.
PR 13-NOV-1989; 89US-0435780.
PR 13-NOV-1990; 90US-0614161.
XX
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
PI Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J, Haber DA;
PI Rose EA, Housman DE, Bruneing W, Darveau A;
XX
DR WPI; 2002-690126/74.
DR N-PSDB; ABS53730.
XX
PT Treating cancer or precancerous condition associated with the Wilms'
PT tumour gene in individual, by administering polypeptide or polypeptide
PT encoded by Wilms' tumour DNA -
XX
PS Example 2; Fig 7; 41pp; English.
XX
CC The present invention relates to a new method of treating cancer or
CC precancerous condition associated with the Wilms' tumour gene. The method
CC of the invention is useful for treating a cancer or precancerous
CC condition associated with the Wilms' tumour gene in an individual, where
CC the cancer or precancerous condition is Wilms' tumour, leukaemia,
CC testicular cancer or ovarian cancer. The present amino acid sequence
CC represents the mouse Wilms' tumour (WT) WTI protein that was used in the
CC methods of the invention.
XX
SQ Sequence 449 AA;
XX
Query Match 100.0%; Score 51; DB 23; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134
XX
RESULT 52
ABG33373
ID ABG33373 standard; Protein; 449 AA.
XX
AC ABG33373;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human WTI.
XX
KW Human; mouse; cytostatic; immunostimulant; WTI; cancer;
KW immune response.
XX
OS Homo sapiens.
XX
EN WO200228414-A1.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US31139.
XX
PR 06-OCT-2000; 2000US-0684361.
PR 09-OCT-2000; 2000US-0685830.
PR 15-FEB-2001; 2001US-0785019.
PR 24-AUG-2001; 2001US-0938864.
XX
PA (CORI-) CORIXA CORP.
PA (GAI/) GAIGER A.
XX
PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
PI Sleath PR, Moseman S, Evans L, Spies AG, Boydston J;
XX
DR WPI; 2002-352217/38.

```

```

XX Novel isolated WTI polynucleotide, and encoded polypeptide, useful for
PT treating and diagnosing cancer in a patient -
XX
PS Example 4; Figure 1; 260pp; English.
XX
CC The invention relates to an isolated WTI polynucleotide (I) and
CC polypeptide encoded by (I). The WTI polynucleotides and polypeptides
CC are used for treating and detecting cancer in a patient, and for
CC stimulating an immune response in patient. ABG33070-ABG33405
CC represent WTI amino acid sequences of the invention.
XX
SQ Sequence 449 AA;
XX
Query Match 100.0%; Score 51; DB 23; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RMPFNAPYL 9
Db 126 RMPFNAPYL 134
XX
RESULT 53
ABG33374
ID ABG33374 standard; Protein; 449 AA.
XX
AC ABG33374;
XX
DT 15-JUL-2002 (first entry)
XX
DE Mouse WTI.
XX
KW Human; mouse; cytostatic; immunostimulant; WTI; cancer;
KW immune response.
XX
OS Mus musculus.
XX
EN WO200228414-A1.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US31139.
XX
PR 06-OCT-2000; 2000US-0684361.
PR 09-OCT-2000; 2000US-0685830.
PR 15-FEB-2001; 2001US-0785019.
PR 24-AUG-2001; 2001US-0938864.
XX
PA (CORI-) CORIXA CORP.
PA (GAI/) GAIGER A.
XX
PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
PI Sleath PR, Moseman S, Evans L, Spies AG, Boydston J;
XX
DR WPI; 2002-352217/38.
XX
PT Novel isolated WTI polynucleotide, and encoded polypeptide, useful for
PT treating and diagnosing cancer in a patient -
XX
PS Example 4; Figure 1; 260pp; English.
XX
CC The invention relates to an isolated WTI polynucleotide (I) and
CC polypeptide encoded by (I). The WTI polynucleotides and polypeptides
CC are used for treating and detecting cancer in a patient, and for
CC stimulating an immune response in patient. ABG33070-ABG33405
CC represent WTI amino acid sequences of the invention.
XX
SQ Sequence 449 AA;
XX
Query Match 100.0%; Score 51; DB 23; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 RMFPNAPYL 9  
 DB 126 RMFPNAPYL 134

RESULT 54  
 ABG33396  
 ID ABG33396 standard; Protein; 449 AA.

AC ABG33396;  
 XX 15-JUL-2002 (first entry)  
 DT  
 XX Human WT1 protein.  
 DE  
 XX Human; mouse; cyclostatic; immunostimulant; WT1; cancer;  
 KM immune response.  
 KW  
 XX Homo sapiens.

OS  
 XX WO200228414-A1.  
 XX 11-APR-2002.  
 PD  
 XX 03-OCT-2001; 2001WO-US31139.  
 PF  
 XX 06-OCT-2000; 2000US-0684361.  
 PR 09-OCT-2000; 2000US-0685830.  
 PR 15-FEB-2001; 2001US-0785019.  
 PR 24-AUG-2001; 2001US-0938864.

XX (CORI-) CORIXA CORP.  
 PA (GAIG/) GAIGER A.

PI Gager A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;  
 PI Sleath PR, Moseman S, Evans U, Spies AG, Boydston J;  
 DR N-PSDB; ABK69676.  
 XX WPI; 2002-352217/38.

PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for  
 PT treating and diagnosing cancer in a patient -  
 PT  
 PS Claim 2; Page 250-251; 260pp; English.  
 CC The invention relates to an isolated WT1 polynucleotide (I) and  
 CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides  
 CC are used for treating and detecting cancer in a patient, and for  
 CC stimulating an immune response in patient. ABG33070-ABG33405  
 CC represent WT1 amino acid sequences of the invention.  
 CC  
 XX Sequence 449 AA;

QY Query Match 100.0%; Score 51; DB 23; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 0.18; 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
 DB 126 RMFPNAPYL 134

RESULT 55  
 AAG78444  
 ID AAG78444 standard; Protein; 449 AA.

AC AAG78444;  
 XX 12-APR-2002 (first entry)  
 DT  
 XX Murine WT1 Wilm's tumour protein.  
 DE  
 XX

KW Tumour; oncogene; retinoblastoma; zinc finger;  
 KM Wilm's tumour disease; WT1; mouse.  
 XX  
 XX Mus sp.  
 OS  
 XX Key Location/Qualifiers  
 FH Domain 317..438  
 FT /label= zinc\_finger\_domains

XX US6316599-B1.  
 XX 13-NOV-2001.  
 PD  
 XX 09-MAR-1998; 98US-0037179.  
 PF  
 XX 02-AUG-1993; 93US-0102942.  
 PR 13-NOV-1989; 89US-0435780.  
 PR 13-NOV-1990; 90US-0614161.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.  
 PA  
 XX Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J, Haber DA;  
 PI Rose EA, Housman DE, Breuning W, Darveau A;  
 DR WPI; 2002-074379/10.  
 DR N-PSDB; AAH99946.

XX Antibodies specific for Wilm's tumour (WT) protein variant WT33, useful  
 PT in immunoassays to detect WT33 in samples and diagnose e.g. Sporadic  
 PT Wilm's tumours -  
 XX  
 PS Example 4; Fig 9; 45pp; English.

XX This invention relates to an isolated antibody specific for a protein  
 CC encoded by a Wilm's tumour DNA. The antibodies may be used in  
 CC immunoassays to detect the presence of the Wilm's tumour variant WT33 in  
 CC biological samples. They may be used in this way to diagnose sporadic  
 CC Wilm's tumours, as seen in Wilm's tumour. The antibody makes it possible  
 CC to detect proteins encoded by DNA which is clearly derived from the 11p13  
 CC Wilm's tumour gene. This is particularly valuable because the treatment  
 CC of Wilm's tumour represents one of the clearest examples of success in  
 CC paediatric oncology, as a result of the development of effective  
 CC therapeutic regimens. A diagnostic test would allow early detection of  
 CC the disease. The presence of the disease can be confirmed, thus making  
 CC it possible to intervene therapeutically prior to or at an earlier  
 CC stage in the development of the disease. This sequence represents  
 CC the WT1 Wilm's tumour protein.  
 CC  
 XX Sequence 449 AA;

QY Query Match 100.0%; Score 51; DB 23; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 0.18; 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
 DB 126 RMFPNAPYL 134

RESULT 56  
 AAG78446  
 ID AAG78446 standard; Protein; 449 AA.

AC AAG78446;  
 XX 12-APR-2002 (first entry)  
 DT  
 XX Predicted WT1 Wilm's tumour polypeptide of humans.  
 DE  
 XX Tumour; oncogene; retinoblastoma; chromosome 11p13; zinc finger;  
 KM Wilm's tumour disease; WT1; human.  
 KW  
 XX Homo sapiens.

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XX  US6316599-B1.
PN
XX  13-NOV-2001.
PD
XX  09-MAR-1998; 98US-0037179.
PF
XX  02-AUG-1993; 93US-0102942.
PR  13-NOV-1989; 89US-0435780.
PR  13-NOV-1990; 90US-0614161.
XX
XX  (MASI ) MASSACHUSETTS INST TECHNOLOGY.
PA
PI  Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J, Haber DA;
PI  Rose EA, Housman DE, Brenning W, Darveau A;
XX
XX  WPI; 2002-074379/10.
DR
XX
XX  Antibodies specific for Wilms' tumour (WT) protein variant WT33, useful
PT  in immunoassays to detect WT33 in samples and diagnose e.g. Sporadic
PT  Wilms' tumours
XX
XX  Disclosure; Fig 10; 45pp; English.
PS
XX
XX  This invention relates to an isolated antibody specific for a protein
CC  encoded by a Wilms' tumour DNA. The antibodies may be used in
CC  immunoassays to detect the presence of the Wilms' tumour variant WT33 in
CC  biological samples. They may be used in this way to diagnose sporadic
CC  Wilms' tumours, as seen in Wilms' tumour. The antibody makes it possible
CC  to detect proteins encoded by DNA which is clearly derived from the 11p13
CC  Wilms' tumour gene. This is particularly valuable because the treatment
CC  of Wilms' tumour represents one of the clearest examples of success in
CC  paediatric oncology, as a result of the development of effective
CC  therapeutic regimens. A diagnostic test would allow early detection of
CC  the disease. The presence of the disease can be confirmed, thus making
CC  it possible to intervene therapeutically prior to or at an earlier
CC  stage in the development of the disease. This sequence represents
CC  the predicted WT1 Wilms' tumour protein of humans.
XX
XX  Sequence 449 AA;
SQ
XX
XX  Query Match 100.0%; Score 51; DB 23; Length 449;
XX  Best Local Similarity 100.0%; Pred. No. 0.18;
XX  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY
XX  1 RMFPNAPYL 9
XX  |||||
XX  126 RMFPNAPYL 134
Db
XX
XX  RESULT 57
XX  ABG71421
XX  ID ABG71421 standard; Protein; 449 AA.
XX
XX  ABG71421;
AC
XX  10-FEB-2003 (first entry)
DT
XX
XX  Murine Wilms' tumour gene WT1 polypeptide.
DE
XX
XX  Mouse; Wilms' tumour gene; WT1; cytostatic; Wilms' tumour; leukaemia;
KM  testicular cancer; ovarian cancer.
XX
XX  Mus sp.
OS
XX
XX  US2002128196-A1.
PN
XX
XX  12-SEP-2002.
PD
XX
XX  12-NOV-2001; 2001US-0993215.
PF
XX
XX  02-AUG-1993; 93US-0102942.
PR  09-MAR-1998; 98US-0037179.
PR  09-MAR-1998; 98US-0037179.
XX

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PR  13-NOV-1989; 89US-0435780.
PR  13-NOV-1990; 90US-0614161.
XX
XX  (MASI ) MASSACHUSETTS INST TECHNOLOGY.
PA
XX
XX  Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J, Haber DA;
PI  Rose EA, Housman DE, Brenning W, Darveau A;
XX
XX  WPI; 2003-066910/06.
DR
XX
XX  N-PSDB; ABS57420.
DR
XX
XX  Pharmaceutical composition for treating cancer or precancerous
PT  condition such as Wilms' tumor, leukemia, testicular and ovarian cancer
PT  associated with Wilms' tumor gene, and for inducing immune and antibody
PT  responses
XX
XX  Example 2; Fig 7; 41pp; English.
PS
XX
XX  The invention relates to a pharmaceutical composition comprising a
CC  polypeptide encoded by a Wilms' tumour gene. The composition is useful
CC  for treating cancer or precancerous conditions (such as Wilms' tumour,
CC  leukemia, testicular and ovarian cancer) associated with the Wilms'
CC  tumour gene in an individual, for inducing an immune response which
CC  results in antibody production in a mammal, and for inducing an antibody
CC  response by administering the composition to the mammal. This sequence
CC  represents a murine Wilms' tumour gene polypeptide, WT1.
XX
XX  Sequence 449 AA;
SQ
XX
XX  Query Match 100.0%; Score 51; DB 24; Length 449;
XX  Best Local Similarity 100.0%; Pred. No. 0.18;
XX  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY
XX  1 RMFPNAPYL 9
XX  |||||
XX  126 RMFPNAPYL 134
Db
XX
XX  RESULT 58
XX  ABG71423
XX  ID ABG71423 standard; Protein; 449 AA.
XX
XX  ABG71423;
AC
XX  10-FEB-2003 (first entry)
DT
XX
XX  Human Wilms' tumour gene WT1 polypeptide.
DE
XX
XX  Human; Wilms' tumour gene; WT1; cytostatic; Wilms' tumour; leukaemia;
KM  testicular cancer; ovarian cancer.
XX
XX  Homo sapiens.
OS
XX
XX  US2002128196-A1.
PN
XX
XX  12-SEP-2002.
PD
XX
XX  12-NOV-2001; 2001US-0993215.
PF
XX
XX  02-AUG-1993; 93US-0102942.
PR  09-MAR-1998; 98US-0037179.
PR  13-NOV-1989; 89US-0435780.
PR  13-NOV-1990; 90US-0614161.
XX
XX  (MASI ) MASSACHUSETTS INST TECHNOLOGY.
PA
XX
XX  Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J, Haber DA;
PI  Rose EA, Housman DE, Brenning W, Darveau A;
XX
XX  WPI; 2003-066910/06.
DR
XX
XX  Pharmaceutical composition for treating cancer or precancerous
PT  condition such as Wilms' tumor, leukemia, testicular and ovarian cancer

```

PT associated with Wlms' tumor gene, and for inducing immune and antibody responses -

XX Disclosure; Fig 8; 41pp; English.

XX The invention relates to a pharmaceutical composition comprising a polypeptide encoded by a Wlms' tumor gene. The composition is useful for treating cancer or precancerous conditions (such as Wlms' tumour, leukaemia, testicular and ovarian cancer) associated with the Wlms' tumour gene in an individual, for inducing an immune response which results in antibody production in a mammal, and for inducing an antibody response by administering the composition to the mammal. This sequence represents a human Wlms' tumour gene polypeptide, WT1.

XX Sequence 449 AA;

SQ

Query Match 100.0%; Score 51; DB 24; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 |||||  
 126 RMFPNAPYL 134

Db

RESULT 59  
 ABB99880  
 ID ABB99880 standard; protein; 449 AA.  
 XX  
 AC ABB99880;  
 XX  
 DT 27-JAN-2003 (first entry)  
 XX  
 DE Mouse Wlms' tumour antigen WT1.  
 XX  
 KW Mouse; murine; Wlms' tumour antigen; WT1; modified WT1 peptide; vaccine; immunotherapy; cancer; leukemia; solid tumour.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 235..243  
 TT /note= "Corresponds to SEQ ID NO:2 (ABB99881)"

PN WO200279253-A1.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 22-MAR-2002; 2002WO-JP02794.  
 XX  
 PR 22-MAR-2001; 2001JP-0083250.  
 XX  
 PA (SUGI/) SUGIYAMA H.  
 XX  
 PI Sugiyama H;  
 XX  
 DR WPI; 2003-046799/04.  
 XX  
 PT Cancer antigen WT1 modified peptides and DNA encoding them for cancer immunotherapy -

XX  
 PS Disclosure; Page 23-25; 30pp; Japanese.

XX The invention relates to modified peptides derived from the murine Wlms' tumor antigen WT1 (ABB99880). The peptides of the invention are 9-30 amino acids long and comprise the sequence Cys-Tyr-Thr-Tyr-Asn-Gln-Met-Asn-Ileu (ABB99882). Cancer vaccines comprising modified WT1 peptides of the invention or DNA encoding them, and antigen presenting cells (including cytotoxic T-cells) which present a peptide of the invention (including complexed with a major histocompatibility complex (MHC) class I molecule, can be used in the immunotherapy of leukemia and solid tumours such as cancers of the bladder, colon, breast, liver, skin, stomach, prostate, testis, lung and uterus. The present sequence represents

CC murine WT1.  
 XX  
 SQ Sequence 449 AA;

Query Match 100.0%; Score 51; DB 24; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 |||||  
 126 RMFPNAPYL 134

Db

RESULT 60  
 ABG33401  
 ID ABG33401 standard; Protein; 495 AA.  
 XX  
 AC ABG33401;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Human WT1-LAMP fusion construct.  
 XX  
 KW Human; mouse; cytostatic; immunostimulant; WT1; cancer; immune response.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200228414-A1.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 03-OCT-2001; 2001WO-US31139.  
 XX  
 PR 06-OCT-2000; 2000US-0684361.  
 PR 09-OCT-2000; 2000US-0685830.  
 PR 15-FEB-2001; 2001US-0785019.  
 PR 24-AUG-2001; 2001US-0938664.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI (GAIG/) GAIGER A.  
 XX  
 PI Galger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;  
 PI Sleath PR, Moseman S, Evans L, Spies AG, Boyston J;  
 XX  
 DR WPI; 2002-352217/38.  
 XX  
 DR N-PSDB; ABR69678.  
 XX  
 PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for treating and diagnosing cancer in a patient -

XX  
 PS Claim 2; Page 256-257; 260pp; English.

XX The invention relates to an isolated WT1 polynucleotide (I) and polypeptide encoded by (I). The WT1 polynucleotides and polypeptides are used for treating and detecting cancer in a patient, and for stimulating an immune response in patient. ABG33070-ABG33405 represent WT1 amino acid sequences of the invention.

XX  
 SQ Sequence 495 AA;

Query Match 100.0%; Score 51; DB 23; Length 495;  
 Best Local Similarity 100.0%; Pred. No. 0.2; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 |||||  
 153 RMFPNAPYL 161

Db

RESULT 61  
 ABG33402  
 ID ABG33402 standard; Protein; 504 AA.

```

XX AC ABG33402;
XX DT 15-JUL-2002 (first entry)
XX DE Human WT1-ubiquitin fusion construct.
XX KW Human; mouse; cytostatic; immunostimulant; WT1; cancer;
XX KW immune response.
XX OS Homo sapiens.
XX PN WO200228414-A1.
XX PD 11-APR-2002.
XX PF 03-OCT-2001; 2001WO-US31139.
XX PR 06-OCT-2000; 2000US-0684361.
XX PR 09-OCT-2000; 2000US-0685830.
XX PR 15-FEB-2001; 2001US-0785019.
XX PR 24-AUG-2001; 2001US-0938864.
XX PA (CORI-) CORIXA CORP.
XX PA (GAI/ ) GAIGER A.
XX PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
XX PI Sleath PR, Mosseman S, Evans L, Spies AG, Boydston J;
XX DR WPI; 2002-352217/38.
XX DR N-PSDB; ABK69681.
XX PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
XX PT treating and diagnosing cancer in a patient -
XX PS Claim 2; Page 257-258; 260pp; English.
XX CC The invention relates to an isolated WT1 polynucleotide (I) and
XX CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides
XX CC are used for treating and detecting cancer in a patient, and for
XX CC stimulating an immune response in patient. ABG33070-ABG33405
XX CC represent WT1 amino acid sequences of the invention.
XX SQ Sequence 504 AA;

Query Match 100.0%; Score 51; DB 23; Length 504;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9
Db 201 RMFPNAPYL 209

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RESULT 62  
ABG33392  
ID ABG33392 standard; Protein; 568 AA.

```

XX AC ABG33392;
XX DT 15-JUL-2002 (first entry)
XX DE Human Ra12/WT1.
XX KW Human; mouse; cytostatic; immunostimulant; WT1; cancer;
XX KW immune response.
XX OS Homo sapiens.
XX PN WO200228414-A1.
XX PD 11-APR-2002.
XX

```

```

PF 03-OCT-2001; 2001WO-US31139.
XX 06-OCT-2000; 2000US-0684361.
XX 09-OCT-2000; 2000US-0685830.
XX 15-FEB-2001; 2001US-0785019.
XX 24-AUG-2001; 2001US-0938864.
XX PA (CORI-) CORIXA CORP.
XX PA (GAI/ ) GAIGER A.
XX PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
XX PI Sleath PR, Mosseman S, Evans L, Spies AG, Boydston J;
XX DR WPI; 2002-352217/38.
XX DR N-PSDB; ABK69686.
XX PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
XX PT treating and diagnosing cancer in a patient -
XX PS Claim 2; Page 243-245; 260pp; English.
XX CC The invention relates to an isolated WT1 polynucleotide (I) and
XX CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides
XX CC are used for treating and detecting cancer in a patient, and for
XX CC stimulating an immune response in patient. ABG33070-ABG33405
XX CC represent WT1 amino acid sequences of the invention.
XX SQ Sequence 568 AA;

Query Match 100.0%; Score 51; DB 23; Length 568;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9
Db 265 RMFPNAPYL 273

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RESULT 63  
AAO22140  
ID AAO22140 standard; Protein; 577 AA.

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XX AC AAO22140;
XX DT 03-OCT-2002 (first entry)
XX DE Ra12-WT1 fusion protein.
XX KW Ra12; serine protease antigen; Mtb32A; Mycobacterium tuberculosis;
XX KW vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
XX KW immunogen; cytokine.
XX OS Chimeric - Unidentified.
XX PN WO200125401-A2.
XX PD 12-APR-2001.
XX PF 06-OCT-2000; 2000WO-US27652.
XX PR 07-OCT-1999; 99US-0158585.
XX PA (CORI-) CORIXA CORP.
XX PI Skeiky Y, Guderian J;
XX PI Sleath PR, Mosseman S, Evans L, Spies AG, Boydston J;
XX DR WPI; 2001-266299/27.
XX DR N-PSDB; AAL40771.
XX PT Recombinant nucleic acid molecule for producing high yield expression
XX PT of desired fusion polypeptides, encodes fusion polypeptide comprising
XX PT Mycobacterium tuberculosis coding sequence and heterologous polypeptide
XX

```

XX PS Disclosure; Fig 4; 39pp; English.

XX CC The invention relates to a recombinant nucleic acid molecule encoding a

CC fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14

CC kDa C-terminal fragment of serine protease antigen MT32A of

CC Mycobacterium tuberculosis, and a heterologous polynucleotide sequence.

CC The recombinant fusion nucleic acids and polypeptides are useful for

CC providing stable and high yield expression of fusion polypeptides of both

CC eukaryotic and prokaryotic origin and to encode a protein product for use

CC as an antigen for detecting serum antibodies. The presence of serum

CC antibodies to M. tuberculosis antigens in an individual indicates that

CC the individual is infected with it. The fusion polypeptides are useful as

CC sources of proteins for monitoring binding of serum antibodies to fusion

CC proteins and as an immunogen to induce and/or enhance immune responses.

CC The coding sequences can be ligated with a coding sequence of another

CC molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and

CC can be used in vivo as a DNA vaccine. This sequence represents the

CC Ral2-WT1 fusion protein relating to the invention.

XX SQ Sequence 577 AA;

Query Match 100.0%; Score 51; DB 22; Length 577;

Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMFPNAPYL 9

Db 275 RMFPNAPYL 283

RESULT 64

ABG33383

ID ABG33383 standard; Protein; 591 AA.

XX AC ABG33383;

XX DT 15-JUL-2002 (first entry)

XX DE Human Trx-WT1.

XX KW Human; mouse; cytosolic; immunostimulant; WT1; cancer;

XX KW immune response.

XX OS Homo sapiens.

XX PN WO200228414-A1.

XX PD 11-APR-2002.

XX PF 03-OCT-2001; 2001WO-US31139.

XX PR 06-OCT-2000; 2000US-0684361.

XX PR 09-OCT-2000; 2000US-0685830.

XX PR 15-PEB-2001; 2001US-0785019.

XX PR 24-AUG-2001; 2001US-0938864.

XX PA (CORI-) CORIXA CORP.

XX PA (GAIG/) GAIGER A.

XX PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;

XX PI Sleath PR, Mossman S, Evans U, Spies AG, Boydston J;

XX DR WPI; 2002-352217/38.

XX DR N-PSDB; A8K69665.

XX PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for

XX PT treating and diagnosing cancer in a patient -

XX PS Claim 2; Page 22-223; 260pp; English.

XX CC The invention relates to an isolated WT1 polynucleotide (I) and

XX CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides

CC are used for treating and detecting cancer in a patient, and for

CC stimulating an immune response in patient. ABG33070-ABG33405

CC represent WT1 amino acid sequences of the invention.

XX SQ Sequence 591 AA;

Query Match 100.0%; Score 51; DB 23; Length 591;

Best Local Similarity 100.0%; Pred. No. 0.24;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMFPNAPYL 9

Db 288 RMFPNAPYL 296

RESULT 65

AAG62154

ID AAG62154 standard; Protein; 692 AA.

XX AC AAG62154;

XX DT 06-JUL-2001 (first entry)

XX DE Human WT1/PSA fusion protein SEQ ID NO: 357.

XX KW Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;

XX KW chromosome 11p13; zinc finger transcription factor.

XX OS Homo sapiens.

XX PN WO200125273-A2.

XX PD 12-APR-2001.

XX PF 04-OCT-2000; 2000WO-US27465.

XX PR 04-OCT-1999; 99US-0157459.

XX PR (CORI-) CORIXA CORP.

XX PA (CORI-) CORIXA CORP.

XX PI Skeiky YAW, Xu J, Cheever MA, Reed SG;

XX PI WPI; 2001-328324/34.

XX DR 04-OCT-2000; 2001WO-US31139.

XX PF 03-OCT-2001; 2001WO-US31139.

XX PR 06-OCT-2000; 2000US-0684361.

XX PR 09-OCT-2000; 2000US-0685830.

XX PR 15-PEB-2001; 2001US-0785019.

XX PR 24-AUG-2001; 2001US-0938864.

XX PA (CORI-) CORIXA CORP.

XX PA (GAIG/) GAIGER A.

XX PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;

XX PI Sleath PR, Mossman S, Evans U, Spies AG, Boydston J;

XX DR WPI; 2002-352217/38.

XX DR N-PSDB; A8K69665.

XX PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for

XX PT treating and diagnosing cancer in a patient -

XX PS Claim 2; Page 22-223; 260pp; English.

XX CC The invention relates to an isolated WT1 polynucleotide (I) and

XX CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides



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## OM protein - protein search, using sw model

Run on: January 21, 2004, 09:02:27 ; Search time 33 Seconds

(without alignments)  
55.768 Million cell updates/sec

Title: US-09-625-963A-1

Perfect score: 51

Sequence: 1 RMPNPAYL 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 762491 seqs, 204481190 residues

Total number of hits satisfying chosen parameters: 179

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 500 summaries

## Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep.\*  
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17: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	9	10	US-09-872-832-46
2	51	100.0	9	11	US-09-938-864-185
3	51	100.0	9	11	US-09-938-864-293
4	51	100.0	9	11	US-09-791-477-185
5	51	100.0	9	11	US-09-791-477-293
6	51	100.0	9	11	US-09-785-019-185
7	51	100.0	9	11	US-09-785-019-293
8	51	100.0	9	12	US-10-210-148-54
9	51	100.0	9	12	US-10-195-835-185
10	51	100.0	9	12	US-10-195-835-293
11	51	100.0	9	12	US-10-286-333-185
12	51	100.0	9	12	US-10-286-333-293
13	51	100.0	9	12	US-10-244-830-185
14	51	100.0	9	12	US-10-244-830-293
15	51	100.0	9	15	US-10-125-635A-185

16	51	100.0	9	15	US-10-125-635A-293	Sequence 293, App
17	51	100.0	9	15	US-10-002-603-185	Sequence 185, App
18	51	100.0	9	15	US-10-002-603-293	Sequence 293, App
19	51	100.0	23	11	US-09-938-864-2	Sequence 2, App11
20	51	100.0	23	11	US-09-938-864-3	(Sequence 2, App11
21	51	100.0	23	11	US-09-791-477-2	Sequence 2, App11
22	51	100.0	23	11	US-09-791-477-3	Sequence 3, App11
23	51	100.0	23	11	US-09-785-019-2	Sequence 2, App11
24	51	100.0	23	11	US-09-785-019-3	Sequence 2, App11
25	51	100.0	23	12	US-10-195-835-2	Sequence 2, App11
26	51	100.0	23	12	US-10-195-835-3	Sequence 2, App11
27	51	100.0	23	12	US-10-286-333-2	Sequence 2, App11
28	51	100.0	23	12	US-10-286-333-3	Sequence 2, App11
29	51	100.0	23	12	US-10-244-830-2	Sequence 2, App11
30	51	100.0	23	12	US-10-244-830-3	Sequence 2, App11
31	51	100.0	23	15	US-10-125-635A-2	Sequence 2, App11
32	51	100.0	23	15	US-10-125-635A-3	Sequence 2, App11
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34	51	100.0	23	15	US-10-002-603-3	Sequence 2, App11
35	51	100.0	152	11	US-09-938-864-343	Sequence 343, App
36	51	100.0	152	11	US-09-785-019-343	Sequence 343, App
37	51	100.0	152	12	US-10-195-835-343	Sequence 343, App
38	51	100.0	152	12	US-10-286-333-343	Sequence 343, App
39	51	100.0	152	12	US-10-244-830-343	Sequence 343, App
40	51	100.0	152	15	US-10-125-635A-343	Sequence 343, App
41	51	100.0	152	15	US-10-002-603-343	Sequence 343, App
42	51	100.0	154	9	US-09-929-315-5	Sequence 5, App11
43	51	100.0	154	10	US-09-938-864-395	Sequence 395, App
44	51	100.0	214	12	US-10-195-835-395	Sequence 395, App
45	51	100.0	214	12	US-10-286-333-395	Sequence 395, App
46	51	100.0	214	12	US-10-244-830-395	Sequence 395, App
47	51	100.0	214	12	US-10-125-635A-395	Sequence 395, App
48	51	100.0	214	15	US-10-002-603-395	Sequence 395, App
49	51	100.0	214	15	US-09-938-864-335	Sequence 335, App
50	51	100.0	256	11	US-09-785-019-335	Sequence 335, App
51	51	100.0	256	11	US-09-785-019-335	Sequence 335, App
52	51	100.0	256	12	US-10-195-835-335	Sequence 335, App
53	51	100.0	256	12	US-10-286-333-335	Sequence 335, App
54	51	100.0	256	12	US-10-244-830-335	Sequence 335, App
55	51	100.0	256	15	US-10-125-635A-335	Sequence 335, App
56	51	100.0	256	15	US-10-002-603-335	Sequence 335, App
57	51	100.0	270	12	US-10-286-333-478	Sequence 478, App
58	51	100.0	270	12	US-10-286-333-502	Sequence 502, App
59	51	100.0	274	12	US-10-286-333-480	Sequence 480, App
60	51	100.0	278	12	US-10-286-333-483	Sequence 483, App
61	51	100.0	280	12	US-10-195-835-461	Sequence 461, App
62	51	100.0	280	12	US-10-286-333-461	Sequence 461, App
63	51	100.0	280	12	US-10-244-830-461	Sequence 461, App
64	51	100.0	280	15	US-10-125-635A-461	Sequence 461, App
65	51	100.0	281	15	US-10-286-333-465	Sequence 465, App
66	51	100.0	281	12	US-10-244-830-465	Sequence 465, App
67	51	100.0	291	12	US-10-286-333-464	Sequence 464, App
68	51	100.0	291	12	US-10-244-830-464	Sequence 464, App
69	51	100.0	292	12	US-10-286-333-470	Sequence 470, App
70	51	100.0	292	12	US-10-286-333-499	Sequence 499, App
71	51	100.0	307	12	US-10-286-333-482	Sequence 482, App
72	51	100.0	310	12	US-10-286-333-481	Sequence 481, App
73	51	100.0	321	12	US-10-195-835-455	Sequence 455, App
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75	51	100.0	321	12	US-10-286-333-479	Sequence 479, App
76	51	100.0	321	12	US-10-286-333-455	Sequence 455, App
77	51	100.0	321	15	US-10-125-635A-455	Sequence 455, App
78	51	100.0	344	11	US-09-938-864-391	Sequence 391, App
79	51	100.0	344	12	US-10-195-835-391	Sequence 391, App
80	51	100.0	344	12	US-10-286-333-391	Sequence 391, App
81	51	100.0	344	12	US-10-244-830-391	Sequence 391, App
82	51	100.0	344	15	US-10-125-635A-391	Sequence 391, App
83	51	100.0	344	15	US-10-002-603-391	Sequence 391, App
84	51	100.0	345	9	US-09-929-315-2	Sequence 2, App11
85	51	100.0	345	10	US-09-938-864-394	Sequence 394, App
86	51	100.0	352	11	US-10-195-835-394	Sequence 394, App
87	51	100.0	352	12	US-10-286-333-394	Sequence 394, App
88	51	100.0	362	12	US-10-286-333-394	Sequence 394, App

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RESULT 1
US-09-872-832-46
; Sequence 46, Application US/09872832
; Patent No. US20020131960A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: 830002-2003.1
; CURRENT APPLICATION NUMBER: US/09/872,832
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/209,157
; PRIOR FILING DATE: 2000-02-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-832-46

Query Match          100.0%; Score 51; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

CY      1 RMPFNAPYL 9
Db      1 RMPFNAPYL 9

RESULT 2
US-09-938-664-185
; Sequence 185, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTL
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413

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SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 185  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-938-864-185

Query Match 100.0%; Score 51; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 1 RMFPNAPYL 9

## RESULT 3

US-09-938-864-293  
Sequence 293, Application US/09938864  
Publication No. US20030072767A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Smithgall, Molly  
APPLICANT: Moulton, Gus  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Mossman, Sally  
APPLICANT: Evans, Lawrence  
APPLICANT: Spies, A. Gregory  
APPLICANT: Boydston, Jeremy  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
FILE REFERENCE: 210121.465C5  
CURRENT APPLICATION NUMBER: US/09/938, 864  
CURRENT FILING DATE: 2001-08-24  
NUMBER OF SEQ ID NOS: 413  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 293  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-938-864-293

Query Match 100.0%; Score 51; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 1 RMFPNAPYL 9

## RESULT 4

US-09-791-477-185  
Sequence 185, Application US/09791477  
Publication No. US20030082194A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS  
TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA  
FILE REFERENCE: 2077.000200  
CURRENT APPLICATION NUMBER: US/09/791,477  
CURRENT FILING DATE: 2001-02-22  
PRIOR APPLICATION NUMBER: 60/184,070  
PRIOR FILING DATE: 2000-02-22  
NUMBER OF SEQ ID NOS: 326  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 185  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-791-477-185

Query Match 100.0%; Score 51; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 1 RMFPNAPYL 9

## RESULT 5

US-09-791-477-293  
Sequence 293, Application US/09791477  
Publication No. US20030082194A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS  
TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA  
FILE REFERENCE: 2077.000200  
CURRENT APPLICATION NUMBER: US/09/791,477  
CURRENT FILING DATE: 2001-02-22  
PRIOR APPLICATION NUMBER: 60/184,070  
PRIOR FILING DATE: 2000-02-22  
NUMBER OF SEQ ID NOS: 326  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 293  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-791-477-293

Query Match 100.0%; Score 51; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 1 RMFPNAPYL 9

## RESULT 6

US-09-785-019-185  
Sequence 185, Application US/09785019  
Publication No. US20030082196A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Cheever, Martin A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Smithgall, Molly  
APPLICANT: Moulton, Gus  
APPLICANT: Vedvick, Thomas S.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
FILE REFERENCE: 210121.465C4  
CURRENT APPLICATION NUMBER: US/09/785,019  
CURRENT FILING DATE: 2001-02-15  
NUMBER OF SEQ ID NOS: 376  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 185  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-785-019-185

Query Match 100.0%; Score 51; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 1 RMFPNAPYL 9

```
Db      1 RMFPNAPYL 9

RESULT 7
US-09-785-019-293
; Sequence 293, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-785-019-293

Query Match      100.0%; Score 51; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6,7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 RMFPNAPYL 9
        |||||
        1 RMFPNAPYL 9

RESULT 8
US-10-210-148-54
; Sequence 54, Application US/10210148
; Publication No. US20030171280A1
; GENERAL INFORMATION:
; APPLICANT: Soderstrom, Karl Petter
; TITLE OF INVENTION: Compositions And Methods For Modulation Of Immune Response
; FILE REFERENCE: TROM0002
; CURRENT APPLICATION NUMBER: US/10/210.148
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: PCT/US02/24311
; PRIOR FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-148-54

Query Match      100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6,7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 RMFPNAPYL 9
        |||||
        1 RMFPNAPYL 9

RESULT 9
US-10-195-835-185
; Sequence 185, Application US/10195835
; Publication No. US20030198622A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.

Db      1 RMFPNAPYL 9

Query Match      100.0%; Score 51; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6,7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 RMFPNAPYL 9
        |||||
        1 RMFPNAPYL 9

RESULT 10
US-10-195-835-293
; Sequence 293, Application US/10195835
; Publication No. US20030198622A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Moesman, Sally P.
; APPLICANT: Evans, Lawrence S.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C8
; CURRENT APPLICATION NUMBER: US/10/195.835
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-195-835-185

Query Match      100.0%; Score 51; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6,7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 RMFPNAPYL 9
        |||||
        1 RMFPNAPYL 9

RESULT 11
US-10-286-333-185
; Sequence 185, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Jaya, No. US20030215458A1a11e
```

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
;; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
;; FILE REFERENCE: 210121.465C10  
;; CURRENT APPLICATION NUMBER: US/10/286.333  
;; CURRENT FILING DATE: 2002-10-30  
;; NUMBER OF SEQ ID NOS: 506  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 185  
;; LENGTH: 9  
;; TYPE: PRT  
;; ORGANISM: Homo sapien  
US-10-286-333-185

Query Match                    100.0%; Score 51; DB 12; Length 9;  
Best Local Similarity       100.0%; Pred. No. 6.7e+05;  
Matches       9; Conservative       0; Mismatches       0; Indels       0; Gaps       0;  
Qy                    1 RMFPNAPYL 9  
                     |||||  
Db                    1 RMFPNAPYL 9

RESULT 12  
US-10-286-333-293  
; Sequence 293, Application US/10286333  
; Publication No. US20030215458A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Jaya, No. US20030215458A1a1e  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
; FILE REFERENCE: 210121.465C10  
; CURRENT APPLICATION NUMBER: US/10/286.333  
; CURRENT FILING DATE: 2002-10-30  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 293  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-286-333-293

Query Match                    100.0%; Score 51; DB 12; Length 9;  
Best Local Similarity       100.0%; Pred. No. 6.7e+05;  
Matches       9; Conservative       0; Mismatches       0; Indels       0; Gaps       0;  
Qy                    1 RMFPNAPYL 9  
                     |||||  
Db                    1 RMFPNAPYL 9

RESULT 13  
US-10-244-830-185  
; Sequence 185, Application US/10244830  
; Publication No. US20030235557A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Cheever, Martin A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
; FILE REFERENCE: 210121.465C9  
; CURRENT APPLICATION NUMBER: US/10/244.830  
; CURRENT FILING DATE: 2002-09-16  
; NUMBER OF SEQ ID NOS: 468  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 185  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-244-830-185

Query Match                    100.0%; Score 51; DB 12; Length 9;

Best Local Similarity       100.0%; Pred. No. 6.7e+05;  
Matches       9; Conservative       0; Mismatches       0; Indels       0; Gaps       0;

Qy                    1 RMFPNAPYL 9  
                     |||||  
Db                    1 RMFPNAPYL 9

RESULT 14  
US-10-244-830-293  
; Sequence 293, Application US/10244830  
; Publication No. US20030235557A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Cheever, Martin A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
; FILE REFERENCE: 210121.465C9  
; CURRENT APPLICATION NUMBER: US/10/244.830  
; CURRENT FILING DATE: 2002-09-16  
; NUMBER OF SEQ ID NOS: 468  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 293  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-244-830-293

Query Match                    100.0%; Score 51; DB 12; Length 9;  
Best Local Similarity       100.0%; Pred. No. 6.7e+05;  
Matches       9; Conservative       0; Mismatches       0; Indels       0; Gaps       0;

Qy                    1 RMFPNAPYL 9  
                     |||||  
Db                    1 RMFPNAPYL 9

RESULT 15  
US-10-125-635A-185  
; Sequence 185, Application US/10125635A  
; Publication No. US20030039635A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Smithgall, Molly D.  
; APPLICANT: Carter, Darick  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Sutherland, R. Alec  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
; FILE REFERENCE: 210121.465C7  
; CURRENT APPLICATION NUMBER: US/10/125.635A  
; CURRENT FILING DATE: 2002-07-19  
; NUMBER OF SEQ ID NOS: 461  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 185  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-125-635A-185

Query Match                    100.0%; Score 51; DB 15; Length 9;  
Best Local Similarity       100.0%; Pred. No. 6.7e+05;  
Matches       9; Conservative       0; Mismatches       0; Indels       0; Gaps       0;

Qy                    1 RMFPNAPYL 9  
                     |||||  
Db                    1 RMFPNAPYL 9

RESULT 16  
US-10-125-635A-293  
; Sequence 293, Application US/10125635A

```
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125.635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-125-635A-293
```

```
Query Match          100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 RMFPNAPYL 9
Db 1 RMFPNAPYL 9
```

## RESULT 17

```
US-10-002-603-185
; Sequence 185, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedavick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002.603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 185
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-002-603-185
```

```
Query Match          100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 RMFPNAPYL 9
Db 1 RMFPNAPYL 9
```

```
RESULT 18
US-10-002-603-293
; Sequence 293, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander.
```

```
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedavick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002.603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-002-603-293
```

```
Query Match          100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 RMFPNAPYL 9
Db 1 RMFPNAPYL 9
```

## RESULT 19

```
US-09-938-864-2
; Sequence 2, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedavick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938.864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-2
```

```
Query Match          100.0%; Score 51; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 RMFPNAPYL 9
Db 10 RMFPNAPYL 18
```

```
RESULT 20
US-09-938-864-3
; Sequence 3, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-938-864-3

Query Match          100.0%; Score 51; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9
   |||||
Db 10 RMFPNAPYL 18

RESULT 21
US-09-791-477-2
; Sequence 2, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-2

Query Match          100.0%; Score 51; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9
   |||||
Db 10 RMFPNAPYL 18

RESULT 22
US-09-791-477-3
; Sequence 3, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: 2077.000200
```

```

; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-477-3

Query Match          100.0%; Score 51; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9
   |||||
Db 10 RMFPNAPYL 18

RESULT 23
US-09-785-019-2
; Sequence 2, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-785-019-2

Query Match          100.0%; Score 51; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9
   |||||
Db 10 RMFPNAPYL 18

RESULT 24
US-09-785-019-3
; Sequence 3, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
```

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 3  
LENGTH: 23  
TYPE: PRT

ORGANISM: Mus musculus  
US-09-785-019-3

Query Match 100.0%; Score 51; DB 11; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
|||  
Db 10 RMFPNAPYL 18

RESULT 25

US-10-195-835-2  
Sequence 2, Application US/10195835  
Publication No. US20030198622A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander  
APPLICANT: Smithgall, Molly D.  
APPLICANT: Carter, Darick  
APPLICANT: Cheever, Martin A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Sutherland, R. Alec  
APPLICANT: Moseman, Sally P.  
APPLICANT: Evans, Lawrence S.  
APPLICANT: Swanson, Ryan M.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1

FILE REFERENCE: 210121.465C8

CURRENT APPLICATION NUMBER: US/10/195,835

CURRENT FILING DATE: 2002-07-12

NUMBER OF SEQ ID NOS: 461

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2  
LENGTH: 23  
TYPE: PRT

ORGANISM: Homo sapien  
US-10-195-835-2

Query Match 100.0%; Score 51; DB 12; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
|||  
Db 10 RMFPNAPYL 18

RESULT 26

US-10-195-835-3  
Sequence 3, Application US/10195835  
Publication No. US20030198622A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander  
APPLICANT: Smithgall, Molly D.  
APPLICANT: Carter, Darick  
APPLICANT: Cheever, Martin A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Sutherland, R. Alec  
APPLICANT: Moseman, Sally P.  
APPLICANT: Evans, Lawrence S.  
APPLICANT: Swanson, Ryan M.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1

FILE REFERENCE: 210121.465C8

CURRENT APPLICATION NUMBER: US/10/195,835

CURRENT FILING DATE: 2002-07-12

NUMBER OF SEQ ID NOS: 461

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 3  
LENGTH: 23  
TYPE: PRT

ORGANISM: Mus musculus  
US-10-195-835-3

Query Match 100.0%; Score 51; DB 12; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
|||  
Db 10 RMFPNAPYL 18

RESULT 27

US-10-286-333-2  
Sequence 2, Application US/10286333  
Publication No. US20030215458A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Jaya, No. US20030215458A1a1ie  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
FILE REFERENCE: 210121.465C10  
CURRENT APPLICATION NUMBER: US/10/286,333  
CURRENT FILING DATE: 2002-10-30  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2  
LENGTH: 23  
TYPE: PRT

ORGANISM: Homo sapien  
US-10-286-333-2

Query Match 100.0%; Score 51; DB 12; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
|||  
Db 10 RMFPNAPYL 18

RESULT 28

US-10-286-333-3  
Sequence 3, Application US/10286333  
Publication No. US20030215458A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Jaya, No. US20030215458A1a1ie  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
FILE REFERENCE: 210121.465C10  
CURRENT APPLICATION NUMBER: US/10/286,333  
CURRENT FILING DATE: 2002-10-30  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 3  
LENGTH: 23  
TYPE: PRT

ORGANISM: Mus musculus  
US-10-286-333-3

Query Match 100.0%; Score 51; DB 12; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
|||  
Db 10 RMFPNAPYL 18



## RESULT 29

US-10-244-830-2  
 ; Sequence 2, Application US/10244830  
 ; Publication No. US20030235557A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Cheever, Martin A.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; FILE REFERENCE: 210121.465C9  
 ; CURRENT APPLICATION NUMBER: US/10/244.830  
 ; CURRENT FILING DATE: 2002-09-16  
 ; NUMBER OF SEQ ID NOS: 468  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 23  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 US-10-244-830-2

Query Match 100.0%; Score 51; DB 12; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 0.019;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
 |||||  
 Db 10 RMFPNAPYL 18

## RESULT 30

US-10-244-830-3  
 ; Sequence 3, Application US/10244830  
 ; Publication No. US20030235557A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Cheever, Martin A.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; FILE REFERENCE: 210121.465C9  
 ; CURRENT APPLICATION NUMBER: US/10/244.830  
 ; CURRENT FILING DATE: 2002-09-16  
 ; NUMBER OF SEQ ID NOS: 468  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 23  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-244-830-3

Query Match 100.0%; Score 51; DB 12; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 0.019;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
 |||||  
 Db 10 RMFPNAPYL 18

## RESULT 31

US-10-125-635A-2  
 ; Sequence 2, Application US/10125635A  
 ; Publication No. US20030039635A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Smithgall, Molly D.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Cheever, Martin A.  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Sutherland, R. Alec  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY

FILE REFERENCE: 210121.465C7  
 ; CURRENT APPLICATION NUMBER: US/10/125.635A  
 ; CURRENT FILING DATE: 2002-07-19  
 ; NUMBER OF SEQ ID NOS: 461  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 23  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 US-10-125-635A-2

Query Match 100.0%; Score 51; DB 15; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 0.019;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
 |||||  
 Db 10 RMFPNAPYL 18

## RESULT 32

US-10-125-635A-3  
 ; Sequence 3, Application US/10125635A  
 ; Publication No. US20030039635A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Smithgall, Molly D.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Cheever, Martin A.  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Sutherland, R. Alec  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; FILE REFERENCE: 210121.465C7  
 ; CURRENT APPLICATION NUMBER: US/10/125.635A  
 ; CURRENT FILING DATE: 2002-07-19  
 ; NUMBER OF SEQ ID NOS: 461  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 23  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-125-635A-3

Query Match 100.0%; Score 51; DB 15; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 0.019;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
 |||||  
 Db 10 RMFPNAPYL 18

## RESULT 33

US-10-002-603-2  
 ; Sequence 2, Application US/10002603  
 ; Publication No. US20030095971A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Smithgall, Molly  
 ; APPLICANT: Moulton, Gus  
 ; APPLICANT: Vedvick, Thomas S.  
 ; APPLICANT: Sleath, Paul R.  
 ; APPLICANT: Mosman, Sally  
 ; APPLICANT: Evans, Lawrence  
 ; APPLICANT: Spies, A. Gregory  
 ; APPLICANT: Boydston, Jeremy  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
 ; FILE REFERENCE: 210121.465C6  
 ; CURRENT APPLICATION NUMBER: US/10/002.603  
 ; CURRENT FILING DATE: 2001-10-30

```
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-002-603-2
```

```
Query Match          100.0%; Score 51; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RMFPNAPYL 9
Db 10 RMFPNAPYL 18
```

## RESULT 34

```
US-10-002-603-3
; Sequence 3, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-002-603-3
```

```
Query Match          100.0%; Score 51; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RMFPNAPYL 9
Db 10 RMFPNAPYL 18
```

## RESULT 35

```
US-09-938-864-343
; Sequence 343, Application US/09938864
; Publication No. US2003007267A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
```

```
; CURRENT FILING DATE: 2001-08-24
```

```
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-864-343
```

```
Query Match          100.0%; Score 51; DB 11; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RMFPNAPYL 9
Db 51 RMFPNAPYL 59
```

## RESULT 36

```
US-09-785-019-343
; Sequence 343, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-019-343
```

```
Query Match          100.0%; Score 51; DB 11; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RMFPNAPYL 9
Db 51 RMFPNAPYL 59
```

## RESULT 37

```
US-10-195-835-343
; Sequence 343, Application US/10195835
; Publication No. US20030198622A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Derrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Mossman, Sally P.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C8
; CURRENT APPLICATION NUMBER: US/10/195,835
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
```

SEQ ID NO 343  
LENGTH: 152  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-195-835-343

Query Match 100.0%; Score 51; DB 12; Length 152;  
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
|||||  
Db 51 RMFPNAPYL 59

RESULT 38  
US-10-286-333-343  
Sequence 343, Application US/10286333  
Publication No. US20030215458A1  
GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Jaya, No. US20030215458A1a1ie  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C10  
CURRENT APPLICATION NUMBER: US/10/286,333  
CURRENT FILING DATE: 2002-10-30  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 343  
LENGTH: 152  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-286-333-343

Query Match 100.0%; Score 51; DB 12; Length 152;  
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
|||||  
Db 51 RMFPNAPYL 59

RESULT 39  
US-10-244-830-343  
Sequence 343, Application US/10244830  
Publication No. US20030235557A1  
GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C9  
CURRENT APPLICATION NUMBER: US/10/244,830  
CURRENT FILING DATE: 2002-09-16  
NUMBER OF SEQ ID NOS: 468  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 343  
LENGTH: 152  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-244-830-343

Query Match 100.0%; Score 51; DB 12; Length 152;  
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
|||||  
Db 51 RMFPNAPYL 59

RESULT 40  
US-10-125-635A-343  
Sequence 343, Application US/10125635A  
Publication No. US20030039635A1  
GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander  
APPLICANT: Saltgall, Molly D.  
APPLICANT: Carter, Darrick  
APPLICANT: Cheever, Martin A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Sutherland, R. Alec  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C7  
CURRENT APPLICATION NUMBER: US/10/125,635A  
CURRENT FILING DATE: 2002-07-19  
NUMBER OF SEQ ID NOS: 461  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 343  
LENGTH: 152  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-125-635A-343

Query Match 100.0%; Score 51; DB 15; Length 152;  
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
|||||  
Db 51 RMFPNAPYL 59

RESULT 41  
US-10-002-603-343  
Sequence 343, Application US/10002603  
Publication No. US30030095971A1  
GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Saltgall, Molly  
APPLICANT: Moulton, Gus  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Kossman, Sally  
APPLICANT: Evans, Lawrence  
APPLICANT: Spies, A. Gregory  
APPLICANT: Boydston, Jeremy  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C6  
CURRENT APPLICATION NUMBER: US/10/002,603  
CURRENT FILING DATE: 2001-10-30  
NUMBER OF SEQ ID NOS: 413  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 343  
LENGTH: 152  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-002-603-343

Query Match 100.0%; Score 51; DB 15; Length 152;  
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
|||||  
Db 51 RMFPNAPYL 59

RESULT 42  
US-09-929-315-5

```
Sequence 5, Application US/09929315
Patent No. US20020082394A1
GENERAL INFORMATION:
APPLICANT: Call, Katherine M.
APPLICANT: Glaser, Thomas M.
APPLICANT: Ito, Caryn Y.
APPLICANT: Buckler, Alan J.
APPLICANT: Pelletier, Jerry
APPLICANT: Haber, Daniel A.
APPLICANT: Rose, Elise A.
APPLICANT: Housman, David E.
APPLICANT: Bruening, Wendy
APPLICANT: Darveau, Andre
TITLE OF INVENTION: Localization and Characterization of the
FILE REFERENCE: 0050.1312-013
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 09/037,179
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: US 08/102,942
PRIOR FILING DATE: 1993-08-02
PRIOR APPLICATION NUMBER: US 07/614,161
PRIOR FILING DATE: 1990-11-13
PRIOR APPLICATION NUMBER: US 07/795,323
PRIOR FILING DATE: 1991-11-20
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 154
TYPE: PRT
ORGANISM: Homo sapien
US-09-929-315-5

Query Match          100.0%; Score 51; DB 9; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 RMFPNAPYL 9
         |||||
Db      40 RMFPNAPYL 48
```

```
RESULT 43
US-09-993-215-5
Sequence 5, Application US/0993215
Patent No. US20020128196A1
GENERAL INFORMATION:
APPLICANT: Call, Katherine M.
APPLICANT: Glaser, Thomas M.
APPLICANT: Ito, Caryn Y.
APPLICANT: Buckler, Alan J.
APPLICANT: Pelletier, Jerry
APPLICANT: Haber, Daniel A.
APPLICANT: Rose, Elise A.
APPLICANT: Housman, David E.
APPLICANT: Bruening, Wendy
APPLICANT: Darveau, Andre
TITLE OF INVENTION: Localization and Characterization of the
FILE REFERENCE: 0050.1312-014
CURRENT FILING DATE: 2001-11-12
PRIOR APPLICATION NUMBER: US 09/037,179
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: US 08/102,942
PRIOR FILING DATE: 1993-08-02
PRIOR APPLICATION NUMBER: US 07/614,161
PRIOR FILING DATE: 1990-11-13
PRIOR APPLICATION NUMBER: US 07/435,780
PRIOR FILING DATE: 1989-11-13
```

```
PRIOR APPLICATION NUMBER: US 07/795,323
PRIOR FILING DATE: 1991-11-20
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 154
TYPE: PRT
ORGANISM: Homo sapien
US-09-993-215-5
```

```
Query Match          100.0%; Score 51; DB 10; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 RMFPNAPYL 9
         |||||
Db      40 RMFPNAPYL 48
```

```
RESULT 44
US-09-938-864-395
Sequence 395, Application US/09938864
Publication No. US20030072767A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: McNeill, Patricia D.
APPLICANT: Smithgall, Molly
APPLICANT: Moulton, Gus
APPLICANT: Vedvick, Thomas S.
APPLICANT: Sleath, Paul R.
APPLICANT: Moorman, Sally
APPLICANT: Evans, Lawrence
APPLICANT: Spies, A. Gregory
APPLICANT: Boydston, Jeremy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTL
FILE REFERENCE: 210121.465C5
CURRENT FILING DATE: 2001-08-24
CURRENT APPLICATION NUMBER: US/09/938,864
NUMBER OF SEQ ID NOS: 413
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 395
LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapiens
US-09-938-864-395
```

```
Query Match          100.0%; Score 51; DB 11; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 RMFPNAPYL 9
         |||||
Db      59 RMFPNAPYL 67
```

```
RESULT 45
US-10-195-835-395
Sequence 395, Application US/10195835
Publication No. US20030198622A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Smithgall, Molly D.
APPLICANT: Carter, Darrick
APPLICANT: Cheever, Martin A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Sutherland, R. Alec
APPLICANT: Moorman, Sally P.
APPLICANT: Evans, Lawrence S.
APPLICANT: Swanson, Ryan M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTL
FILE REFERENCE: 210121.465C8
```

CURRENT APPLICATION NUMBER: US/10/195,835  
CURRENT FILING DATE: 2002-07-12  
NUMBER OF SEQ ID NOS: 461  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 395  
LENGTH: 214  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-195-835-395

Query Match 100.0%; Score 51; DB 12; Length 214;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
Db 59 RMFPNAPYL 67

RESULT 46  
US-10-286-333-395  
Sequence 395, Application US/10286333  
Publication No. US20030215458A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C10  
CURRENT APPLICATION NUMBER: US/10/286,333  
CURRENT FILING DATE: 2002-10-30  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 395  
LENGTH: 214  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-286-333-395

Query Match 100.0%; Score 51; DB 12; Length 214;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
Db 59 RMFPNAPYL 67

RESULT 47  
US-10-244-830-395  
Sequence 395, Application US/10244830  
Publication No. US20030235557A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C9  
CURRENT APPLICATION NUMBER: US/10/244,830  
CURRENT FILING DATE: 2002-09-16  
NUMBER OF SEQ ID NOS: 468  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 395  
LENGTH: 214  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-244-830-395

Query Match 100.0%; Score 51; DB 12; Length 214;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
Db 59 RMFPNAPYL 67

RESULT 48  
US-10-125-635A-395  
Sequence 395, Application US/10125635A  
Publication No. US20030039635A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Smithgall, Molly D.  
APPLICANT: Carter, Darick  
APPLICANT: Cheever, Martin A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C7  
CURRENT APPLICATION NUMBER: US/10/125,635A  
CURRENT FILING DATE: 2002-07-19  
NUMBER OF SEQ ID NOS: 461  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 395  
LENGTH: 214  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-125-635A-395

Query Match 100.0%; Score 51; DB 15; Length 214;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
Db 59 RMFPNAPYL 67

RESULT 49  
US-10-002-603-395  
Sequence 395, Application US/10002603  
Publication No. US20030095971A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Smithgall, Molly  
APPLICANT: Moulton, Gus  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Mossman, Sally  
APPLICANT: Evans, Lawrence  
APPLICANT: Spies, A. Gregory  
APPLICANT: Boydston, Jeremy  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C6  
CURRENT APPLICATION NUMBER: US/10/002,603  
CURRENT FILING DATE: 2001-10-30  
NUMBER OF SEQ ID NOS: 413  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 395  
LENGTH: 214  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-002-603-395

Query Match 100.0%; Score 51; DB 15; Length 214;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
Db 59 RMFPNAPYL 67

```

RESULT 50
US-09-938-864-335
; Sequence 335, Application US/09938864
; Publication No. US2003007267A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-864-335

```

```

Query Match      100.0%; Score 51; DB 11; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RMFPNAPYL 9
Db 133 RMFPNAPYL 141

```

```

RESULT 51
US-09-785-019-335
; Sequence 335, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-019-335

```

```

Query Match      100.0%; Score 51; DB 11; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RMFPNAPYL 9
Db 133 RMFPNAPYL 141

```

```

RESULT 52
US-10-195-835-335
; Sequence 335, Application US/10195835
; Publication No. US20030198622A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Mossman, Sally P.
; APPLICANT: Evans, Lawrence S.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C8
; CURRENT APPLICATION NUMBER: US/10/195,835
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-835-335

```

```

Query Match      100.0%; Score 51; DB 12; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RMFPNAPYL 9
Db 133 RMFPNAPYL 141

```

```

RESULT 53
US-10-286-333-335
; Sequence 335, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Java, No. US20030215458A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286,333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-333-335

```

```

Query Match      100.0%; Score 51; DB 12; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RMFPNAPYL 9
Db 133 RMFPNAPYL 141

```

```

RESULT 54
US-10-244-830-335
; Sequence 335, Application US/10244830
; Publication No. US2003023557A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.

```

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244,830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-244-830-335

Query Match
Best Local Similarity 100.0%; Score 51; DB 12; Length 256;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9
Db 133 RMFPNAPYL 141

RESULT 55
US-10-125-635A-335
; Sequence 335, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125,635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-635A-335

Query Match
Best Local Similarity 100.0%; Score 51; DB 15; Length 256;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9
Db 133 RMFPNAPYL 141

RESULT 56
US-10-002-603-335
; Sequence 335, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C6
```

```

; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-603-335

Query Match
Best Local Similarity 100.0%; Score 51; DB 15; Length 256;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9
Db 133 RMFPNAPYL 141

RESULT 57
US-10-286-333-478
; Sequence 478, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Daya, No. US20030215458A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286,333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 478
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-333-478

Query Match
Best Local Similarity 100.0%; Score 51; DB 12; Length 267;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9
Db 112 RMFPNAPYL 120

RESULT 58
US-10-286-333-502
; Sequence 502, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Daya, No. US20030215458A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286,333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 502
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-333-502

Query Match
Best Local Similarity 100.0%; Score 51; DB 12; Length 270;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 RMFPNAPYL 9  
 Db 115 RMFPNAPYL 123

RESULT 59  
 US-10-286-333-480  
 ; Sequence 480, Application US/10286333  
 ; Publication No. US20030215458A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: McNeill, Patricia D  
 ; APPLICANT: Jaya, No. US20030215458A1a1e  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; FILE REFERENCE: 210121.465C10  
 ; CURRENT APPLICATION NUMBER: US/10/286.333  
 ; CURRENT FILING DATE: 2002-10-30  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 480  
 ; LENGTH: 274  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-286-333-480

Query Match 100.0%; Score 51; DB 12; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 0.23;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 Db 119 RMFPNAPYL 127

RESULT 60  
 US-10-286-333-483  
 ; Sequence 483, Application US/10286333  
 ; Publication No. US20030215458A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: McNeill, Patricia D  
 ; APPLICANT: Jaya, No. US20030215458A1a1e  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; FILE REFERENCE: 210121.465C10  
 ; CURRENT APPLICATION NUMBER: US/10/286.333  
 ; CURRENT FILING DATE: 2002-10-30  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 483  
 ; LENGTH: 278  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-286-333-483

Query Match 100.0%; Score 51; DB 12; Length 278;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 Db 123 RMFPNAPYL 131

RESULT 61  
 US-10-195-835-461  
 ; Sequence 461, Application US/10195835  
 ; Publication No. US20030198622A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Smithgall, Molly D.

APPLICANT: Carter, Darrick  
 APPLICANT: Cheever, Martin A.  
 APPLICANT: McNeill, Patricia D.  
 APPLICANT: Sutherland, R. Alec  
 APPLICANT: Mossman, Sally P.  
 APPLICANT: Evans, Lawrence S.  
 APPLICANT: Swanson, Ryan M.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; FILE REFERENCE: 210121.465C8  
 ; CURRENT APPLICATION NUMBER: US/10/195.835  
 ; CURRENT FILING DATE: 2002-07-12  
 ; NUMBER OF SEQ ID NOS: 461  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 461  
 ; LENGTH: 280  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-195-835-461

Query Match 100.0%; Score 51; DB 12; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 Db 125 RMFPNAPYL 133

RESULT 62  
 US-10-286-333-461  
 ; Sequence 461, Application US/10286333  
 ; Publication No. US20030215458A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Jaya, No. US20030215458A1a1e  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; FILE REFERENCE: 210121.465C10  
 ; CURRENT APPLICATION NUMBER: US/10/286.333  
 ; CURRENT FILING DATE: 2002-10-30  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 461  
 ; LENGTH: 280  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-286-333-461

Query Match 100.0%; Score 51; DB 12; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 Db 125 RMFPNAPYL 133

RESULT 63  
 US-10-244-830-461  
 ; Sequence 461, Application US/10244830  
 ; Publication No. US20030235557A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Cheever, Martin A.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; FILE REFERENCE: 210121.465C9  
 ; CURRENT APPLICATION NUMBER: US/10/244.830  
 ; CURRENT FILING DATE: 2002-09-16  
 ; NUMBER OF SEQ ID NOS: 468  
 ; SOFTWARE: FastSeq for Windows Version 3.0



SEQ ID NO 461  
LENGTH: 280  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-244-830-461

Query Match  
Best Local Similarity 100.0%; Score 51; DB 12; Length 280;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
Db 125 RMFPNAPYL 133

RESULT 64  
US-10-125-635A-461  
Sequence 461, Application US/10125635A  
Publication No. US20030039635A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Smithgall, Molly D.  
APPLICANT: Carter, Darick  
APPLICANT: Cheever, Martin A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Sutherland, R. Alec  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C7  
CURRENT APPLICATION NUMBER: US/10/125, 635A  
CURRENT FILING DATE: 2002-07-19  
NUMBER OF SEQ ID NOS: 461  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 461  
LENGTH: 280  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-125-635A-461

Query Match  
Best Local Similarity 100.0%; Score 51; DB 15; Length 280;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
Db 125 RMFPNAPYL 133

RESULT 65  
US-10-286-333-465  
Sequence 465, Application US/10286333  
Publication No. US20030215458A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Jaya, No. US20030215458A1a1e  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C10  
CURRENT APPLICATION NUMBER: US/10/286, 333  
CURRENT FILING DATE: 2002-10-30  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 465  
LENGTH: 281  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-286-333-465

Query Match  
Best Local Similarity 100.0%; Score 51; DB 12; Length 281;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 66  
US-10-244-830-465  
Sequence 465, Application US/10244830  
Publication No. US20030235557A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C9  
CURRENT APPLICATION NUMBER: US/10/244, 830  
CURRENT FILING DATE: 2002-09-16  
NUMBER OF SEQ ID NOS: 468  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 465  
LENGTH: 281  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-244-830-465

Query Match  
Best Local Similarity 100.0%; Score 51; DB 12; Length 281;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 67  
US-10-286-333-464  
Sequence 464, Application US/10286333  
Publication No. US20030215458A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Jaya, No. US20030215458A1a1e  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C10  
CURRENT APPLICATION NUMBER: US/10/286, 333  
CURRENT FILING DATE: 2002-10-30  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 464  
LENGTH: 291  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-286-333-464

Query Match  
Best Local Similarity 100.0%; Score 51; DB 12; Length 291;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 68  
US-10-244-830-464  
Sequence 464, Application US/10244830  
Publication No. US20030235557A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C9  
CURRENT APPLICATION NUMBER: US/10/244, 830  
CURRENT FILING DATE: 2002-09-16  
NUMBER OF SEQ ID NOS: 468  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 465  
LENGTH: 281  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-244-830-465

Query Match  
Best Local Similarity 100.0%; Score 51; DB 12; Length 281;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FILE REFERENCE: 210121.465C9  
CURRENT APPLICATION NUMBER: US/10/244.830  
CURRENT FILING DATE: 2002-09-16  
NUMBER OF SEQ ID NOS: 468  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 464  
LENGTH: 291  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-244-830-464

Query Match  
Best Local Similarity 100.0%; Score 51; DB 12; Length 291;  
Pred. No. 0.25;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 69  
US-10-286-333-470  
Sequence 470, Application US/10286333  
Publication No. US20030215458A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
FILE REFERENCE: 210121.465C10  
CURRENT APPLICATION NUMBER: US/10/286.333  
CURRENT FILING DATE: 2002-10-30  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 470  
LENGTH: 292  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-286-333-470

Query Match  
Best Local Similarity 100.0%; Score 51; DB 12; Length 292;  
Pred. No. 0.25;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 137 RMFPNAPYL 145

RESULT 70  
US-10-286-333-499  
Sequence 499, Application US/10286333  
Publication No. US20030215458A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
FILE REFERENCE: 210121.465C10  
CURRENT APPLICATION NUMBER: US/10/286.333  
CURRENT FILING DATE: 2002-10-30  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 499  
LENGTH: 292  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-286-333-499

Query Match  
Best Local Similarity 100.0%; Score 51; DB 12; Length 292;  
Pred. No. 0.25;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 137 RMFPNAPYL 145

RESULT 71  
US-10-286-333-482  
Sequence 482, Application US/10286333  
Publication No. US20030215458A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
FILE REFERENCE: 210121.465C10  
CURRENT APPLICATION NUMBER: US/10/286.333  
CURRENT FILING DATE: 2002-10-30  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 482  
LENGTH: 307  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-286-333-482

Query Match  
Best Local Similarity 100.0%; Score 51; DB 12; Length 307;  
Pred. No. 0.26;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 152 RMFPNAPYL 160

RESULT 72  
US-10-286-333-481  
Sequence 481, Application US/10286333  
Publication No. US20030215458A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
FILE REFERENCE: 210121.465C10  
CURRENT APPLICATION NUMBER: US/10/286.333  
CURRENT FILING DATE: 2002-10-30  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 481  
LENGTH: 310  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-286-333-481

Query Match  
Best Local Similarity 100.0%; Score 51; DB 12; Length 310;  
Pred. No. 0.26;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 155 RMFPNAPYL 163

RESULT 73  
US-10-195-835-455  
Sequence 455, Application US/10195835  
Publication No. US20030198622A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander

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; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darriek A.
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Mossman, Sally P.
; APPLICANT: Evans, Lawrence S.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C8
; CURRENT APPLICATION NUMBER: US/10/195,835
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 455
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-835-455

Query Match
Best Local Similarity 100.0%; Score 51; DB 12; Length 321;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9
DB 166 RMFPNAPYL 174

RESULT 74
US-10-286-333-455
; Sequence 455, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Jaya, No. US20030215458A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286,333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 455
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-333-455

Query Match
Best Local Similarity 100.0%; Score 51; DB 12; Length 321;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9
DB 166 RMFPNAPYL 174

RESULT 75
US-10-286-333-479
; Sequence 479, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Jaya, No. US20030215458A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286,333
; CURRENT FILING DATE: 2002-10-30
```

```

; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 479
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-333-479

Query Match
Best Local Similarity 100.0%; Score 51; DB 12; Length 321;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9
DB 166 RMFPNAPYL 174

RESULT 76
US-10-244-830-455
; Sequence 455, Application US/10244830
; Publication No. US2003023557A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244,830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 455
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-244-830-455

Query Match
Best Local Similarity 100.0%; Score 51; DB 12; Length 321;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9
DB 166 RMFPNAPYL 174

RESULT 77
US-10-125-635A-455
; Sequence 455, Application US/10125635A
; Publication No. US2003039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darriek A.
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125,635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 455
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-635A-455

Query Match
Best Local Similarity 100.0%; Score 51; DB 15; Length 321;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 RMFPNAPYL 9  
 Db 166 RMFPNAPYL 174

## RESULT 78

US-09-938-864-391  
 ; Sequence 391, Application US/09938864  
 ; Publication No. US20030072767A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Smithgall, Molly  
 ; APPLICANT: Moulton, Gus  
 ; APPLICANT: Vedvick, Thomas S.  
 ; APPLICANT: Sleath, Paul R.  
 ; APPLICANT: Moseman, Sally  
 ; APPLICANT: Evans, Lawrence  
 ; APPLICANT: Spies, A. Gregory  
 ; APPLICANT: Boydston, Jeremy  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI  
 ; FILE REFERENCE: 210121.465C5  
 ; CURRENT APPLICATION NUMBER: US/09/938,864  
 ; CURRENT FILING DATE: 2001-08-24  
 ; NUMBER OF SEQ ID NOS: 413  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 391  
 ; LENGTH: 344  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-938-864-391

Query Match 100.0%; Score 51; DB 11; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 0.29;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 Db 189 RMFPNAPYL 197

## RESULT 79

US-10-195-835-391  
 ; Sequence 391, Application US/10195835  
 ; Publication No. US20030198622A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Smithgall, Molly D.  
 ; APPLICANT: Carter, Darriek  
 ; APPLICANT: Cheever, Martin A.  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Sutherland, R. Alec  
 ; APPLICANT: Mossman, Sally P.  
 ; APPLICANT: Evans, Lawrence S.  
 ; APPLICANT: Swanson, Ryan M.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI  
 ; FILE REFERENCE: 210121.465C8  
 ; CURRENT APPLICATION NUMBER: US/10/195,835  
 ; CURRENT FILING DATE: 2002-07-12  
 ; NUMBER OF SEQ ID NOS: 461  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 391  
 ; LENGTH: 344  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-195-835-391

Query Match 100.0%; Score 51; DB 12; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 0.29;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 Db 189 RMFPNAPYL 197

## RESULT 80

US-10-286-333-391  
 ; Sequence 391, Application US/10286333  
 ; Publication No. US20030215458A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Java, No. US20030215458A1a1e  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI  
 ; FILE REFERENCE: 210121.465C10  
 ; CURRENT APPLICATION NUMBER: US/10/286,333  
 ; CURRENT FILING DATE: 2002-10-30  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 391  
 ; LENGTH: 344  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-286-333-391

Query Match 100.0%; Score 51; DB 12; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 0.29;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 Db 189 RMFPNAPYL 197

## RESULT 81

US-10-244-830-391  
 ; Sequence 391, Application US/10244830  
 ; Publication No. US20030235557A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Cheever, Martin A.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI  
 ; FILE REFERENCE: 210121.465C9  
 ; CURRENT APPLICATION NUMBER: US/10/244,830  
 ; CURRENT FILING DATE: 2002-09-16  
 ; NUMBER OF SEQ ID NOS: 468  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 391  
 ; LENGTH: 344  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-244-830-391

Query Match 100.0%; Score 51; DB 12; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 0.29;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 Db 189 RMFPNAPYL 197

## RESULT 82

US-10-125-635A-391  
 ; Sequence 391, Application US/10125635A  
 ; Publication No. US20030039635A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Smithgall, Molly D.  
 ; APPLICANT: Carter, Darriek

APPLICANT: Cheever, Martin A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Sutherland, R. Alec  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C7  
CURRENT APPLICATION NUMBER: US/10/125,635A  
CURRENT FILING DATE: 2002-07-19  
NUMBER OF SEQ ID NOS: 461  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 391  
LENGTH: 344  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-125-635A-391

Query Match 100.0%; Score 51; DB 15; Length 344;  
Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 189 RMFPNAPYL 197

RESULT 83  
US-10-002-603-391  
Sequence 391, Application US/10002603  
Publication No. US20030095971A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Smithgall, Molly  
APPLICANT: Moulton, Gus  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Mossman, Sally  
APPLICANT: Evans, Lawrence  
APPLICANT: Spies, A. Gregory  
APPLICANT: Boydston, Jeremy  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C6  
CURRENT APPLICATION NUMBER: US/10/002,603  
CURRENT FILING DATE: 2001-10-30  
NUMBER OF SEQ ID NOS: 413  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 391  
LENGTH: 344  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-002-603-391

Query Match 100.0%; Score 51; DB 15; Length 344;  
Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 189 RMFPNAPYL 197

RESULT 84  
US-09-929-315-2  
Sequence 2, Application US/09929315  
Patent No. US20020082394A1  
GENERAL INFORMATION:  
APPLICANT: Call, Katherine M.  
APPLICANT: Glaser, Thomas M.  
APPLICANT: Ito, Caryn Y.  
APPLICANT: Buckler, Alan J.  
APPLICANT: Pelletier, Jerry  
APPLICANT: Haber, Daniel A.

APPLICANT: Rose, Elise A.  
APPLICANT: Housman, David E.  
APPLICANT: Bruening, Wendy  
APPLICANT: Darveau, Andre  
TITLE OF INVENTION: Localization and Characterization of the  
FILE REFERENCE: 0050.1312-013  
CURRENT APPLICATION NUMBER: US/09/929,315  
CURRENT FILING DATE: 2001-08-14,161  
PRIOR APPLICATION NUMBER: US 09/037,179  
PRIOR FILING DATE: 1998-03-09  
PRIOR APPLICATION NUMBER: US 08/102,942  
PRIOR FILING DATE: 1993-08-02  
PRIOR APPLICATION NUMBER: US 07/614,161  
PRIOR FILING DATE: 1990-11-13  
PRIOR APPLICATION NUMBER: US 07/435,780  
PRIOR FILING DATE: 1989-11-13  
PRIOR APPLICATION NUMBER: US 07/795,323  
PRIOR FILING DATE: 1991-11-20  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-929-315-2

Query Match 100.0%; Score 51; DB 9; Length 345;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 42 RMFPNAPYL 50

RESULT 85  
US-09-993-215-2  
Sequence 2, Application US/09993215  
Patent No. US20020128196A1  
GENERAL INFORMATION:  
APPLICANT: Call, Katherine M.  
APPLICANT: Glaser, Thomas M.  
APPLICANT: Ito, Caryn Y.  
APPLICANT: Buckler, Alan J.  
APPLICANT: Pelletier, Jerry  
APPLICANT: Haber, Daniel A.  
APPLICANT: Rose, Elise A.  
APPLICANT: Housman, David E.  
APPLICANT: Bruening, Wendy  
APPLICANT: Darveau, Andre  
TITLE OF INVENTION: Localization and Characterization of the  
FILE REFERENCE: 0050.1312-014  
CURRENT APPLICATION NUMBER: US/09/993,215  
CURRENT FILING DATE: 2001-11-12,179  
PRIOR APPLICATION NUMBER: US 09/037,179  
PRIOR FILING DATE: 1998-03-09  
PRIOR APPLICATION NUMBER: US 08/102,942  
PRIOR FILING DATE: 1993-08-02  
PRIOR APPLICATION NUMBER: US 07/614,161  
PRIOR FILING DATE: 1990-11-13  
PRIOR APPLICATION NUMBER: US 07/435,780  
PRIOR FILING DATE: 1989-11-13  
PRIOR APPLICATION NUMBER: US 07/795,323  
PRIOR FILING DATE: 1991-11-20  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-993-215-2

Query Match 100.0%; Score 51; DB 10; Length 345;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
|||||  
DB 42 RMFPNAPYL 50

## RESULT 86

US-09-938-864-394  
; Sequence 394, Application US/09938864  
; Publication No. US2003007267A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Smithgall, Molly  
; APPLICANT: Moulton, Gus  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Moosman, Sally  
; APPLICANT: Evans, Lawrence  
; APPLICANT: Spies, A. Gregory  
; APPLICANT: Boydston, Jeremy  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; FILE REFERENCE: 210121.465C5  
; CURRENT APPLICATION NUMBER: US/09/938,864  
; CURRENT FILING DATE: 2001-08-24  
; NUMBER OF SEQ ID NOS: 413  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 394  
; LENGTH: 362  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-938-864-394

Query Match 100.0%; Score 51; DB 11; Length 362;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
|||||  
DB 59 RMFPNAPYL 67

## RESULT 87

US-10-195-835-394  
; Sequence 394, Application US/10195835  
; Publication No. US20030198622A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Smithgall, Molly D.  
; APPLICANT: Carter, Derrick  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Sutherland, R. Alec  
; APPLICANT: Moosman, Sally P.  
; APPLICANT: Evans, Lawrence S.  
; APPLICANT: Swanson, Ryan M.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; FILE REFERENCE: 210121.465C8  
; CURRENT APPLICATION NUMBER: US/10/195,835  
; CURRENT FILING DATE: 2002-07-12  
; NUMBER OF SEQ ID NOS: 461  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 394  
; LENGTH: 362  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-195-835-394

Query Match 100.0%; Score 51; DB 12; Length 362;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
|||||  
DB 59 RMFPNAPYL 67

## RESULT 88

US-10-286-333-394  
; Sequence 394, Application US/10286333  
; Publication No. US20030215458A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Jaya, No. US20030215458A1a1e  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; FILE REFERENCE: 210121.465C10  
; CURRENT APPLICATION NUMBER: US/10/286,333  
; CURRENT FILING DATE: 2002-10-30  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 394  
; LENGTH: 362  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-286-333-394

Query Match 100.0%; Score 51; DB 12; Length 362;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
|||||  
DB 59 RMFPNAPYL 67

RESULT 89  
US-10-244-830-394  
; Sequence 394, Application US/10244830  
; Publication No. US2003023557A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Cheever, Martin A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; FILE REFERENCE: 210121.465C9  
; CURRENT APPLICATION NUMBER: US/10/244,830  
; CURRENT FILING DATE: 2002-09-16  
; NUMBER OF SEQ ID NOS: 468  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 394  
; LENGTH: 362  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-244-830-394

Query Match 100.0%; Score 51; DB 12; Length 362;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
|||||  
DB 59 RMFPNAPYL 67

RESULT 90  
US-10-125-635A-394  
; Sequence 394, Application US/10125635A  
; Publication No. US20030039635A1

```
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125.635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 394
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-635A-394
```

```
Query Match          100.0%; Score 51; DB 15; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RMFPNAPYL 9
Db 59 RMFPNAPYL 67
```

```
RESULT 91
US-10-002-603-394
; Sequence 394, Application US/10002603
; Publication No. US20030095971A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002.603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 394
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-603-394
```

```
Query Match          100.0%; Score 51; DB 15; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RMFPNAPYL 9
Db 59 RMFPNAPYL 67
```

```
RESULT 92
US-09-938-864-346
; Sequence 346, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
```

```
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938.864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 346
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-864-346
```

```
Query Match          100.0%; Score 51; DB 11; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RMFPNAPYL 9
Db 66 RMFPNAPYL 74
```

```
RESULT 93
US-09-785-019-346
; Sequence 346, Application US/09785019
; Publication No. US20030082196A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785.019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 346
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-019-346
```

```
Query Match          100.0%; Score 51; DB 11; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RMFPNAPYL 9
Db 66 RMFPNAPYL 74
```

```
RESULT 94
US-10-195-835-346
; Sequence 346, Application US/10195835
; Publication No. US20030198622A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
```





Query Match 100.0%; Score 51; DB 15; Length 369;  
Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
|||  
Db 66 RMFPNAPYL 74

RESULT 99  
US-09-938-864-333  
; Sequence 333, Application US/09938864  
; Publication No. US2003007267A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Smithgall, Molly  
; APPLICANT: Moulton, Gus  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Moesman, Sally  
; APPLICANT: Evans, Lawrence  
; APPLICANT: Spies, A. Gregory  
; APPLICANT: Boydston, Jeremy  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
; FILE REFERENCE: 210121.465C5  
; CURRENT FILING DATE: 2001-08-24  
; CURRENT FILING DATE: 2001-08-24  
; NUMBER OF SEQ ID NOS: 413  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 333  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-938-864-333

Query Match 100.0%; Score 51; DB 11; Length 410;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
|||  
Db 287 RMFPNAPYL 295

RESULT 100  
US-09-785-019-333  
; Sequence 333, Application US/09785019  
; Publication No. US20030082196A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Smithgall, Molly  
; APPLICANT: Moulton, Gus  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Sleath, Paul  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
; FILE REFERENCE: 210121.465C4  
; CURRENT FILING DATE: 2001-02-15  
; CURRENT FILING DATE: 2001-02-15  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 333  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-785-019-333

Query Match 100.0%; Score 51; DB 11; Length 410;

Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
|||  
Db 287 RMFPNAPYL 295

RESULT 101  
US-10-195-835-333  
; Sequence 333, Application US/10195835  
; Publication No. US20030198622A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Smithgall, Molly D.  
; APPLICANT: Carter, Darick  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Sutherland, R. Alec  
; APPLICANT: Moesman, Sally P.  
; APPLICANT: Evans, Lawrence S.  
; APPLICANT: Swanson, Ryan M.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
; FILE REFERENCE: 210121.465C8  
; CURRENT APPLICATION NUMBER: US/10/195,835  
; CURRENT FILING DATE: 2002-07-12  
; NUMBER OF SEQ ID NOS: 461  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 333  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-195-835-333

Query Match 100.0%; Score 51; DB 12; Length 410;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
|||  
Db 287 RMFPNAPYL 295

RESULT 102  
US-10-286-333-333  
; Sequence 333, Application US/10286333  
; Publication No. US20030215458A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Jaya, No. US20030215458A1  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
; FILE REFERENCE: 210121.465C10  
; CURRENT APPLICATION NUMBER: US/10/286,333  
; CURRENT FILING DATE: 2002-10-30  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 333  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-286-333-333

Query Match 100.0%; Score 51; DB 12; Length 410;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMFPNAPYL 9  
|||  
Db 287 RMFPNAPYL 295

Query Match 100.0%; Score 51; DB 12; Length 410;

```
RESULT 103
US-10-244-830-333
; Sequence 333, Application US/10244830
; Publication No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244,830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-244-830-333

Query Match          100.0%; Score 51; DB 12; Length 410;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RMFPNAPYL 9
        |||||
        |||||
Db      287 RMFPNAPYL 295

RESULT 104
US-10-125-635A-333
; Sequence 333, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick D.
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125,635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-635A-333

Query Match          100.0%; Score 51; DB 15; Length 410;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RMFPNAPYL 9
        |||||
        |||||
Db      287 RMFPNAPYL 295

RESULT 105
US-10-002-603-333
; Sequence 333, Application US/10002603
; Publication No. US2003009597A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
```

```
APPLICANT: Sleath, Paul R.
APPLICANT: Mossman, Sally
APPLICANT: Evans, Lawrence
APPLICANT: Spies, A. Gregory
APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-603-333

Query Match          100.0%; Score 51; DB 15; Length 410;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RMFPNAPYL 9
        |||||
        |||||
Db      287 RMFPNAPYL 295

RESULT 106
US-09-938-864-393
; Sequence 393, Application US/09938864
; Publication No. US2003007267A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 393
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-864-393

Query Match          100.0%; Score 51; DB 11; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RMFPNAPYL 9
        |||||
        |||||
Db      265 RMFPNAPYL 273

RESULT 107
US-10-195-835-393
; Sequence 393, Application US/10195835
; Publication No. US20030198622A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
```

```

; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Mossman, Sally P.
; APPLICANT: Evans, Lawrence S.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C8
; CURRENT APPLICATION NUMBER: US/10/195,835
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 393
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-835-393

```

```

Query Match      100.0%; Score 51; DB 12; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 RMFPNAPYL 9
        |||||
Db      265 RMFPNAPYL 273

```

```

RESULT 108
US-10-286-333-393
; Sequence 393, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Java, No. US20030215458A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286,333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 393
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-333-393

```

```

Query Match      100.0%; Score 51; DB 12; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 RMFPNAPYL 9
        |||||
Db      265 RMFPNAPYL 273

```

```

RESULT 109
US-10-244-830-393
; Sequence 393, Application US/10244830
; Publication No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244,830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 393
; LENGTH: 420

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-244-830-393

```

```

Query Match      100.0%; Score 51; DB 12; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 RMFPNAPYL 9
        |||||
Db      265 RMFPNAPYL 273

```

```

RESULT 110
US-10-125-635A-393
; Sequence 393, Application US/10125635A
; Publication No. US2003039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smitbgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125,635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 393
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-635A-393

```

```

Query Match      100.0%; Score 51; DB 15; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 RMFPNAPYL 9
        |||||
Db      265 RMFPNAPYL 273

```

```

RESULT 111
US-10-002-603-393
; Sequence 393, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smitbgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 393
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-603-393

```

```
Query Match      100.0%; Score 51; DB 15; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.36; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY      1 RMFPNAPYL 9
        |||||
Db      265 RMFPNAPYL 273

RESULT 112
US-09-938-864-405
; Sequence 405, Application US/0993864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleacht, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTL
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938, 864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 405
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-864-405

Query Match      100.0%; Score 51; DB 11; Length 428;
Best Local Similarity 100.0%; Pred. No. 0.37; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY      1 RMFPNAPYL 9
        |||||
Db      126 RMFPNAPYL 134

RESULT 113
US-10-195-835-405
; Sequence 405, Application US/10195835
; Publication No. US20030198622A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Mossman, Sally P.
; APPLICANT: Evans, Lawrence S.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTL
; FILE REFERENCE: 210121.465C8
; CURRENT APPLICATION NUMBER: US/10/195, 835
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 405
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-835-405

Query Match      100.0%; Score 51; DB 12; Length 428;
Best Local Similarity 100.0%; Pred. No. 0.37; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY      1 RMFPNAPYL 9
        |||||
Db      126 RMFPNAPYL 134

RESULT 114
US-10-286-333-405
; Sequence 405, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Java, No. US20030215458A1a11e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTL
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286, 333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 405
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-333-405

Query Match      100.0%; Score 51; DB 12; Length 426;
Best Local Similarity 100.0%; Pred. No. 0.37; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY      1 RMFPNAPYL 9
        |||||
Db      126 RMFPNAPYL 134

RESULT 115
US-10-244-830-405
; Sequence 405, Application US/10244830
; Publication No. US2003023557A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTL
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244, 830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 405
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-244-830-405

Query Match      100.0%; Score 51; DB 12; Length 428;
Best Local Similarity 100.0%; Pred. No. 0.37; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY      1 RMFPNAPYL 9
        |||||
Db      126 RMFPNAPYL 134

RESULT 116
US-10-125-635A-405
; Sequence 405, Application US/10125635A
; Publication No. US20030039635A1
```

GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Smithgall, Molly D.  
APPLICANT: Carter, Darrick  
APPLICANT: Cheever, Martin A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Sutherland, R. Alec  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI  
FILE REFERENCE: 210121.465C7  
CURRENT APPLICATION NUMBER: US/10/125.635A  
CURRENT FILING DATE: 2002-07-19  
NUMBER OF SEQ ID NOS: 461  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 405  
LENGTH: 428  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-125-635A-405

Query Match 100.0%; Score 51; DB 15; Length 428;  
Best Local Similarity 100.0%; Pred. No. 0.37;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 117  
US-10-002-603-405  
Sequence 405, Application US/10002603  
Publication No. US20030095977A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Smithgall, Molly  
APPLICANT: Moulton, Gus  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Mossman, Sally  
APPLICANT: Evans, Lawrence  
APPLICANT: Spies, A. Gregory  
APPLICANT: Boydston, Jeremy  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI  
FILE REFERENCE: 210121.465C6  
CURRENT APPLICATION NUMBER: US/10/002.603  
CURRENT FILING DATE: 2001-10-30  
NUMBER OF SEQ ID NOS: 413  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 405  
LENGTH: 428  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-002-603-405

Query Match 100.0%; Score 51; DB 15; Length 428;  
Best Local Similarity 100.0%; Pred. No. 0.37;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 118  
US-09-938-864-408  
Sequence 408, Application US/09938864  
Publication No. US200300767A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.

APPLICANT: Smithgall, Molly  
APPLICANT: Moulton, Gus  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Mossman, Sally  
APPLICANT: Evans, Lawrence  
APPLICANT: Spies, A. Gregory  
APPLICANT: Boydston, Jeremy  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI  
FILE REFERENCE: 210121.465C5  
CURRENT APPLICATION NUMBER: US/09/938.864  
CURRENT FILING DATE: 2001-08-24  
NUMBER OF SEQ ID NOS: 413  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 408  
LENGTH: 429  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-938-864-408

Query Match 100.0%; Score 51; DB 11; Length 429;  
Best Local Similarity 100.0%; Pred. No. 0.37;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 119  
US-10-195-835-408  
Sequence 408, Application US/10195835  
Publication No. US20030198622A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Smithgall, Molly D.  
APPLICANT: Carter, Darrick  
APPLICANT: Cheever, Martin A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Sutherland, R. Alec  
APPLICANT: Mossman, Sally P.  
APPLICANT: Evans, Lawrence S.  
APPLICANT: Swanson, Ryan M.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI  
FILE REFERENCE: 210121.465C8  
CURRENT APPLICATION NUMBER: US/10/195.835  
CURRENT FILING DATE: 2002-07-12  
NUMBER OF SEQ ID NOS: 461  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 408  
LENGTH: 429  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-195-835-408

Query Match 100.0%; Score 51; DB 12; Length 429;  
Best Local Similarity 100.0%; Pred. No. 0.37;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 120  
US-10-286-333-408  
Sequence 408, Application US/10286333  
Publication No. US20030215458A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.

```

; ORGANISM: Homo sapiens
; US-10-125-635A-408
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286.333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 408
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-286-333-408

```

```

Query Match      100.0%; Score 51; DB 12; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 RMFPNAPYL 9
Db      126 RMFPNAPYL 134

```

```

RESULT 121
; US-10-244-830-408
; Sequence 408, Application US/10244830
; Publication No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244.830
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 408
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-244-830-408

```

```

Query Match      100.0%; Score 51; DB 12; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 RMFPNAPYL 9
Db      126 RMFPNAPYL 134

```

```

RESULT 122
; US-10-125-635A-408
; Sequence 408, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125.635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 408
; LENGTH: 429
; TYPE: PRT

```

```

; ORGANISM: Homo sapiens
; US-10-125-635A-408

```

```

Query Match      100.0%; Score 51; DB 15; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 RMFPNAPYL 9
Db      126 RMFPNAPYL 134

```

```

RESULT 123
; US-10-002-603-408
; Sequence 408, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mosman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydscon, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002.603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 408
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-002-603-408

```

```

Query Match      100.0%; Score 51; DB 15; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 RMFPNAPYL 9
Db      126 RMFPNAPYL 134

```

```

RESULT 124
; US-09-929-315-4
; Sequence 4, Application US/09929315
; Patent No. US20020082394A1
; GENERAL INFORMATION:
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Brunning, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; FILE REFERENCE: 0050.1312-013
; CURRENT APPLICATION NUMBER: US/09/929.315
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 09/037,179
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 08/102,942
; PRIOR FILING DATE: 1993-08-02

```

PRIOR APPLICATION NUMBER: US 07/614,161  
PRIOR FILING DATE: 1990-11-13  
PRIOR APPLICATION NUMBER: US 07/435,780  
PRIOR FILING DATE: 1989-11-13  
PRIOR APPLICATION NUMBER: US 07/795,323  
PRIOR FILING DATE: 1991-11-20  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Murine  
US-09-929-315-4

Query Match 100.0%; Score 51; DB 9; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 125  
US-09-929-315-6  
Sequence 6, Application US/09929315  
Patent No. US20020082394A1  
GENERAL INFORMATION:  
APPLICANT: Glaser, Katherine M.  
APPLICANT: Ito, Caryn Y.  
APPLICANT: Buckler, Alan J.  
APPLICANT: Pelletier, Jerry  
APPLICANT: Haber, Daniel A.  
APPLICANT: Rose, Elise A.  
APPLICANT: Housman, David E.  
APPLICANT: Bruening, Wendy  
TITLE OF INVENTION: Localization and Characterization of the  
FILE REFERENCE: 0050.1312-013  
CURRENT APPLICATION NUMBER: US/09/929,315  
CURRENT FILING DATE: 2001-08-14  
PRIOR APPLICATION NUMBER: US 09/037,179  
PRIOR FILING DATE: 1998-03-09  
PRIOR APPLICATION NUMBER: US 08/102,942  
PRIOR FILING DATE: 1993-08-02  
PRIOR APPLICATION NUMBER: US 07/614,161  
PRIOR FILING DATE: 1990-11-13  
PRIOR APPLICATION NUMBER: US 07/435,780  
PRIOR FILING DATE: 1989-11-13  
PRIOR APPLICATION NUMBER: US 07/795,323  
PRIOR FILING DATE: 1991-11-20  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-929-315-6

Query Match 100.0%; Score 51; DB 9; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 126

US-09-993-215-4  
Sequence 4, Application US/09993215  
Patent No. US20020128196A1  
GENERAL INFORMATION:  
APPLICANT: Call, Katherine M.  
APPLICANT: Glaser, Thomas M.  
APPLICANT: Ito, Caryn Y.  
APPLICANT: Buckler, Alan J.  
APPLICANT: Pelletier, Jerry  
APPLICANT: Haber, Daniel A.  
APPLICANT: Rose, Elise A.  
APPLICANT: Housman, David E.  
APPLICANT: Bruening, Wendy  
TITLE OF INVENTION: Localization and Characterization of the  
FILE REFERENCE: 0050.1312-014  
CURRENT APPLICATION NUMBER: US/09/993,215  
CURRENT FILING DATE: 2001-11-12  
PRIOR APPLICATION NUMBER: US 09/037,179  
PRIOR FILING DATE: 1998-03-09  
PRIOR APPLICATION NUMBER: US 08/102,942  
PRIOR FILING DATE: 1993-08-02  
PRIOR APPLICATION NUMBER: US 07/614,161  
PRIOR FILING DATE: 1990-11-13  
PRIOR APPLICATION NUMBER: US 07/435,780  
PRIOR FILING DATE: 1989-11-13  
PRIOR APPLICATION NUMBER: US 07/795,323  
PRIOR FILING DATE: 1991-11-20  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Murine  
US-09-993-215-4

Query Match 100.0%; Score 51; DB 10; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 127  
US-09-993-215-6  
Sequence 6, Application US/09993215  
Patent No. US20020128196A1  
GENERAL INFORMATION:  
APPLICANT: Call, Katherine M.  
APPLICANT: Glaser, Thomas M.  
APPLICANT: Ito, Caryn Y.  
APPLICANT: Buckler, Alan J.  
APPLICANT: Pelletier, Jerry  
APPLICANT: Haber, Daniel A.  
APPLICANT: Rose, Elise A.  
APPLICANT: Housman, David E.  
APPLICANT: Bruening, Wendy  
TITLE OF INVENTION: Localization and Characterization of the  
FILE REFERENCE: 0050.1312-014  
CURRENT APPLICATION NUMBER: US/09/993,215  
CURRENT FILING DATE: 2001-11-12  
PRIOR APPLICATION NUMBER: US 09/037,179  
PRIOR FILING DATE: 1998-03-09  
PRIOR APPLICATION NUMBER: US 08/102,942  
PRIOR FILING DATE: 1993-08-02  
PRIOR APPLICATION NUMBER: US 07/614,161

PRIOR FILING DATE: 1990-11-13  
PRIOR APPLICATION NUMBER: US 07/435,780  
PRIOR FILING DATE: 1989-11-13  
PRIOR APPLICATION NUMBER: US 07/795,323  
PRIOR FILING DATE: 1991-11-20  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-993-215-6

Query Match 100.0%; Score 51; DB 10; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 128  
US-09-938-864-319  
Sequence 319, Application US/09938864  
Publication No. US20030072767A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Smithgall, Molly  
APPLICANT: Moulton, Gus  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Mossman, Sally  
APPLICANT: Evans, Lawrence  
APPLICANT: Spies, A. Gregory  
APPLICANT: Boydston, Jeremy  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI  
FILE REFERENCE: 210121.465C5  
CURRENT APPLICATION NUMBER: US/09/938,864  
CURRENT FILING DATE: 2001-08-24  
NUMBER OF SEQ ID NOS: 413  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 319  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-938-864-319

Query Match 100.0%; Score 51; DB 11; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 129  
US-09-938-864-320  
Sequence 320, Application US/09938864  
Publication No. US20030072767A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Smithgall, Molly  
APPLICANT: Moulton, Gus  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Mossman, Sally  
APPLICANT: Evans, Lawrence  
APPLICANT: Spies, A. Gregory

APPLICANT: Boydston, Jeremy  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI  
FILE REFERENCE: 210121.465C5  
CURRENT APPLICATION NUMBER: US/09/938,864  
CURRENT FILING DATE: 2001-08-24  
NUMBER OF SEQ ID NOS: 413  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 320  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-938-864-320

Query Match 100.0%; Score 51; DB 11; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 130  
US-09-938-864-404  
Sequence 404, Application US/09938864  
Publication No. US20030072767A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Smithgall, Molly  
APPLICANT: Moulton, Gus  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Mossman, Sally  
APPLICANT: Evans, Lawrence  
APPLICANT: Spies, A. Gregory  
APPLICANT: Boydston, Jeremy  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI  
FILE REFERENCE: 210121.465C5  
CURRENT APPLICATION NUMBER: US/09/938,864  
CURRENT FILING DATE: 2001-08-24  
NUMBER OF SEQ ID NOS: 413  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 404  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-938-864-404

Query Match 100.0%; Score 51; DB 11; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 131  
US-09-791-477-319  
Sequence 319, Application US/09791477  
Publication No. US20030082194A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS  
FILE REFERENCE: 2077.000200  
CURRENT APPLICATION NUMBER: US/09/791,477  
CURRENT FILING DATE: 2001-02-22  
PRIOR APPLICATION NUMBER: 60/184,070



PRIOR FILING DATE: 2000-02-22  
; NUMBER OF SEQ ID NOS: 326  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 319  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-477-319

Query Match  
Best Local Similarity 100.0%; Score 51; DB 11; Length 449;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 132  
US-09-791-477-320  
; Sequence 320, Application US/09791477  
; Publication No. US20030082194A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Cheever, Martin A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS  
; FILE REFERENCE: 2077.000200  
; CURRENT FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/184,070  
; PRIOR FILING DATE: 2000-02-22  
; NUMBER OF SEQ ID NOS: 326  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 320  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-791-477-320

Query Match  
Best Local Similarity 100.0%; Score 51; DB 11; Length 449;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 133  
US-09-785-019-319  
; Sequence 319, Application US/09785019  
; Publication No. US20030082196A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Smithgall, Molly  
; APPLICANT: Moulton, Gus  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Sleath, Paul  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; FILE REFERENCE: 210121.465C4  
; CURRENT FILING DATE: 2001-02-15  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 319  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-785-019-319

Query Match  
Best Local Similarity 100.0%; Score 51; DB 11; Length 449;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 134  
US-09-785-019-320  
; Sequence 320, Application US/09785019  
; Publication No. US20030082196A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Smithgall, Molly  
; APPLICANT: Moulton, Gus  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Sleath, Paul  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; FILE REFERENCE: 210121.465C4  
; CURRENT FILING DATE: 2001-02-15  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 320  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-785-019-320

Query Match  
Best Local Similarity 100.0%; Score 51; DB 11; Length 449;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 135  
US-10-177-390-4  
; Sequence 4, Application US/10177390  
; Publication No. US20030143743A1  
; GENERAL INFORMATION:  
; APPLICANT: Schuler, Gerold  
; APPLICANT: N.V. Antwerp Innovatiecentrum  
; TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with Linear  
; FILE REFERENCE: 021505wo/JH/ml  
; CURRENT FILING DATE: 2002-06-20  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-177-390-4

Query Match  
Best Local Similarity 100.0%; Score 51; DB 12; Length 449;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 136  
 US-10-195-835-319  
 ; Sequence 319, Application US/10195835  
 ; Publication No. US20030198622A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Smithgall, Molly D.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Cheever, Martin A.  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Sutherland, R. Alec  
 ; APPLICANT: Mossman, Sally P.  
 ; APPLICANT: Evans, Lawrence S.  
 ; APPLICANT: Swanson, Ryan M.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; FILE REFERENCE: 210121.465C8  
 ; CURRENT APPLICATION NUMBER: US/10/195,835  
 ; CURRENT FILING DATE: 2002-07-12  
 ; NUMBER OF SEQ ID NOS: 461  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 319  
 ; LENGTH: 449  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 US-10-195-835-319

Query Match 100.0%; Score 51; DB 12; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 0.39;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 Db 126 RMFPNAPYL 134

RESULT 137  
 US-10-195-835-320  
 ; Sequence 320, Application US/10195835  
 ; Publication No. US20030198622A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Smithgall, Molly D.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Cheever, Martin A.  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Sutherland, R. Alec  
 ; APPLICANT: Mossman, Sally P.  
 ; APPLICANT: Evans, Lawrence S.  
 ; APPLICANT: Swanson, Ryan M.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; FILE REFERENCE: 210121.465C8  
 ; CURRENT APPLICATION NUMBER: US/10/195,835  
 ; CURRENT FILING DATE: 2002-07-12  
 ; NUMBER OF SEQ ID NOS: 461  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 320  
 ; LENGTH: 449  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-195-835-320

Query Match 100.0%; Score 51; DB 12; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 0.39;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 Db 126 RMFPNAPYL 134

RESULT 138

US-10-195-835-404  
 ; Sequence 404, Application US/10195835  
 ; Publication No. US20030198622A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Smithgall, Molly D.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Cheever, Martin A.  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Sutherland, R. Alec  
 ; APPLICANT: Mossman, Sally P.  
 ; APPLICANT: Evans, Lawrence S.  
 ; APPLICANT: Swanson, Ryan M.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; FILE REFERENCE: 210121.465C8  
 ; CURRENT APPLICATION NUMBER: US/10/195,835  
 ; CURRENT FILING DATE: 2002-07-12  
 ; NUMBER OF SEQ ID NOS: 461  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 404  
 ; LENGTH: 449  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-195-835-404

Query Match 100.0%; Score 51; DB 12; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 0.39;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 Db 126 RMFPNAPYL 134

RESULT 139  
 US-10-286-333-319  
 ; Sequence 319, Application US/10286333  
 ; Publication No. US20030215458A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Jaya, No. US20030215458A1a1ie  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; FILE REFERENCE: 210121.465C10  
 ; CURRENT APPLICATION NUMBER: US/10/286,333  
 ; CURRENT FILING DATE: 2002-10-30  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 319  
 ; LENGTH: 449  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 US-10-286-333-319

Query Match 100.0%; Score 51; DB 12; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 0.39;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
 Db 126 RMFPNAPYL 134

RESULT 140  
 US-10-286-333-320  
 ; Sequence 320, Application US/10286333  
 ; Publication No. US20030215458A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Jaya, No. US20030215458A1a1ie

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
;; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
;; FILE REFERENCE: 210121.465C10  
;; CURRENT APPLICATION NUMBER: US/10/286.333  
;; CURRENT FILING DATE: 2002-10-30  
;; NUMBER OF SEQ ID NOS: 506  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO: 320  
;; LENGTH: 449  
;; TYPE: PRT  
;; ORGANISM: Mus musculus  
US-10-286-333-320

Query Match 100.0%; Score 51; DB 12; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.39; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

OY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 141  
US-10-286-333-404  
; Sequence 404, Application US/10286333  
; Publication No. US20030215458A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Java, No. US20030215458A1a1ie  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
; FILE REFERENCE: 210121.465C10  
; CURRENT APPLICATION NUMBER: US/10/286.333  
; CURRENT FILING DATE: 2002-10-30  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 404  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-286-333-404

Query Match 100.0%; Score 51; DB 12; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.39; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

OY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 142  
US-10-244-830-319  
; Sequence 319, Application US/10244830  
; Publication No. US20030235557A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Cheever, Martin A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
; FILE REFERENCE: 210121.465C9  
; CURRENT APPLICATION NUMBER: US/10/244.830  
; CURRENT FILING DATE: 2002-09-16  
; NUMBER OF SEQ ID NOS: 468  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 319  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-244-830-319

Query Match 100.0%; Score 51; DB 12; Length 449;

Best Local Similarity 100.0%; Pred. No. 0.39; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

OY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 143  
US-10-244-830-320  
; Sequence 320, Application US/10244830  
; Publication No. US20030235557A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Cheever, Martin A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
; FILE REFERENCE: 210121.465C9  
; CURRENT APPLICATION NUMBER: US/10/244.830  
; CURRENT FILING DATE: 2002-09-16  
; NUMBER OF SEQ ID NOS: 468  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 320  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-244-830-320

Query Match 100.0%; Score 51; DB 12; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.39; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

OY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 144  
US-10-244-830-404  
; Sequence 404, Application US/10244830  
; Publication No. US20030235557A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Cheever, Martin A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
; FILE REFERENCE: 210121.465C9  
; CURRENT APPLICATION NUMBER: US/10/244.830  
; CURRENT FILING DATE: 2002-09-16  
; NUMBER OF SEQ ID NOS: 468  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 404  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-244-830-404

Query Match 100.0%; Score 51; DB 12; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.39; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

OY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 145  
US-10-125-635A-319  
; Sequence 319, Application US/10125635A  
; Publication No. US20030039635A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Smithgall, Molly D.

APPLICANT: Carter, Darick  
APPLICANT: Cheever, Martin A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Sutherland, R. Alec  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C7  
CURRENT APPLICATION NUMBER: US/10/125.635A  
CURRENT FILING DATE: 2002-07-19  
NUMBER OF SEQ ID NOS: 461  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 319  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-125-635A-319

Query Match 100.0%; Score 51; DB 15; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
DB 126 RMFPNAPYL 134

RESULT 146  
US-10-125-635A-320  
Sequence 320, Application US/10125635A  
Publication No. US20030039635A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Smithgall, Molly D.  
APPLICANT: Carter, Darick  
APPLICANT: Cheever, Martin A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Sutherland, R. Alec  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C7  
CURRENT APPLICATION NUMBER: US/10/125.635A  
CURRENT FILING DATE: 2002-07-19  
NUMBER OF SEQ ID NOS: 461  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 320  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-125-635A-320

Query Match 100.0%; Score 51; DB 15; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
DB 126 RMFPNAPYL 134

RESULT 147  
US-10-125-635A-404  
Sequence 404, Application US/10125635A  
Publication No. US20030039635A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Smithgall, Molly D.  
APPLICANT: Carter, Darick  
APPLICANT: Cheever, Martin A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Sutherland, R. Alec  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C7

CURRENT APPLICATION NUMBER: US/10/125.635A  
CURRENT FILING DATE: 2002-07-19  
NUMBER OF SEQ ID NOS: 461  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 404  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-125-635A-404

Query Match 100.0%; Score 51; DB 15; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
DB 126 RMFPNAPYL 134

RESULT 148  
US-10-002-603-319  
Sequence 319, Application US/10002603  
Publication No. US20030095971A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Smithgall, Molly  
APPLICANT: Moulton, Gus  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Mossman, Sally  
APPLICANT: Evans, Lawrence  
APPLICANT: Spies, A. Gregory  
APPLICANT: Boydston, Jeremy  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C6  
CURRENT APPLICATION NUMBER: US/10/002.603  
CURRENT FILING DATE: 2001-10-30  
NUMBER OF SEQ ID NOS: 413  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 319  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-002-603-319

Query Match 100.0%; Score 51; DB 15; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
DB 126 RMFPNAPYL 134

RESULT 149  
US-10-002-603-320  
Sequence 320, Application US/10002603  
Publication No. US20030095971A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Smithgall, Molly  
APPLICANT: Moulton, Gus  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Mossman, Sally  
APPLICANT: Evans, Lawrence  
APPLICANT: Spies, A. Gregory  
APPLICANT: Boydston, Jeremy  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
FILE REFERENCE: 210121.465C7

Wed Jan 21 09:23:38 2004

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FILE REFERENCE: 210121.465C6
CURRENT APPLICATION NUMBER: US/10/002,603
CURRENT FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 413
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 320
LENGTH: 449
TYPE: PRT
ORGANISM: Mus musculus
US-10-002-603-320
```

```
Query Match          100.0%; Score 51; DB 15; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RMFPNAPYL 9
        |||||
Db       126 RMFPNAPYL 134
```

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RESULT 150
US-10-002-603-404
Sequence 404, Application US/10002603
Publication No. US20030095971A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: McNeill, Patricia D.
APPLICANT: Smithgall, Molly
APPLICANT: Moulton, Gus
APPLICANT: Vedvick, Thomas S.
APPLICANT: Sleath, Paul R.
APPLICANT: Mossman, Sally
APPLICANT: Evans, Lawrence
APPLICANT: Spies, A. Gregory
APPLICANT: Boydston, Jeremy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
FILE REFERENCE: 210121.465C6
CURRENT APPLICATION NUMBER: US/10/002,603
CURRENT FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 413
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 404
LENGTH: 449
TYPE: PRT
ORGANISM: Homo sapiens
US-10-002-603-404
```

```
Query Match          100.0%; Score 51; DB 15; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY      1 RMFPNAPYL 9
        |||||
Db       126 RMFPNAPYL 134
```

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Search completed: January 21, 2004, 09:11:50
Job time : 34 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 21, 2004, 08:42:29 ; Search time 22 Seconds  
(without alignments)  
17.309 Million cell updates/sec

Title: US-09-625-963A-1  
Sequence: 1 RMFPNAPYL 9

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTCUS COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	154	1 US-08-102-942A-5	Sequence 5, Appli
2	51	100.0	154	4 US-09-037-179B-5	Sequence 5, Appli
3	51	100.0	210	1 US-08-234-783-2	Sequence 2, Appli
4	51	100.0	210	1 US-08-456-907-2	Sequence 2, Appli
5	51	100.0	210	5 PCT-US95-05523-2	Sequence 2, Appli
6	51	100.0	345	1 US-08-102-942A-2	Sequence 2, Appli
7	51	100.0	345	1 US-09-037-179B-2	Sequence 2, Appli
8	51	100.0	429	1 US-08-234-783-4	Sequence 4, Appli
9	51	100.0	429	1 US-08-456-907-4	Sequence 4, Appli
10	51	100.0	429	5 PCT-US95-05523-4	Sequence 4, Appli
11	51	100.0	449	1 US-08-102-942A-4	Sequence 4, Appli
12	51	100.0	449	1 US-08-102-942A-6	Sequence 6, Appli
13	51	100.0	449	1 US-09-037-179B-4	Sequence 4, Appli
14	51	100.0	449	4 US-09-037-179B-6	Sequence 6, Appli
15	38	74.5	269	4 US-09-257-991A-19580	Sequence 19580, A
16	37	72.5	50	3 US-08-975-080-26	Sequence 26, Appli
17	37	72.5	56	4 US-08-657-759-24	Sequence 24, Appli
18	37	72.5	204	4 US-09-134-001C-2975	Sequence 2975, Ap
19	37	72.5	1151	3 US-08-836-134-23	Sequence 23, Appli
20	37	72.5	1151	4 US-09-493-784-23	Sequence 23, Appli
21	37	72.5	1232	3 US-08-836-134-2	Sequence 2, Appli
22	37	72.5	1232	4 US-09-493-784-2	Sequence 2, Appli
23	36	70.6	67	2 US-08-511-485-23	Sequence 23, Appli
24	36	70.6	67	4 US-09-201-936-23	Sequence 23, Appli
25	36	70.6	217	3 US-08-297-431B-33	Sequence 33, Appli
26	36	70.6	365	4 US-09-818-512-4	Sequence 4, Appli
27	36	70.6	370	3 US-09-150-133-1	Sequence 1, Appli

28	36	70.6	370	3 US-09-150-133-3	Sequence 3, Appli
29	36	70.6	370	3 US-09-150-141-1	Sequence 1, Appli
30	36	70.6	370	3 US-09-150-141-3	Sequence 1, Appli
31	36	70.6	370	3 US-09-374-493-1	Sequence 1, Appli
32	36	70.6	370	3 US-09-374-493-3	Sequence 3, Appli
33	36	70.6	370	3 US-09-374-824-1	Sequence 1, Appli
34	36	70.6	370	3 US-09-374-824-1	Sequence 3, Appli
35	36	70.6	370	3 US-09-374-824-1	Sequence 1, Appli
36	36	70.6	370	3 US-09-374-492-3	Sequence 3, Appli
37	36	70.6	370	4 US-09-849-562A-2	Sequence 2, Appli
38	36	70.6	370	4 US-09-849-031A-2	Sequence 2, Appli
39	36	70.6	376	4 US-09-818-512-2	Sequence 2, Appli
40	36	70.6	389	4 US-08-430-286A-7	Sequence 7, Appli
41	36	70.6	438	5 PCT-US95-05523A-2	Sequence 2, Appli
42	36	70.6	618	2 US-08-511-485-8	Sequence 8, Appli
43	36	70.6	618	2 US-09-212-971-8	Sequence 8, Appli
44	36	70.6	618	3 US-08-800-929A-8	Sequence 8, Appli
45	36	70.6	618	3 US-08-569-749-2	Sequence 2, Appli

## ALIGNMENTS

## RESULT 1

US-08-102-942A-5  
Sequence 5, Application US/08102942A  
Patent No. 5726288

## GENERAL INFORMATION:

APPLICANT: Call, Katherine M.  
APPLICANT: Glaeser, Thomas M.  
APPLICANT: Ito, Caryn Y.  
APPLICANT: Buckler, Alan J.  
APPLICANT: Pelletier, Jerry  
APPLICANT: Haber, Daniel A.  
APPLICANT: Rose, Blise A.  
APPLICANT: Housman, David E.  
APPLICANT: Bruening, Wendy  
APPLICANT: Darveau, Andre  
TITLE OF INVENTION: Localization and Characterization of the  
TITLE OF INVENTION: Wilms' Tumor Gene  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/102,942A  
FILING DATE: 02-AUG-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: MIT-5194A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 154 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-102-942A-5

Query Match 100.0%; Score 51; DB 1; Length 154;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
Db 40 RMFPNAPYL 48

## RESULT 2

US-09-037-179B-5  
Sequence 5, Application US/09037179B  
Patent No. 6316599  
GENERAL INFORMATION:  
APPLICANT: Call, Katherine M.  
APPLICANT: Glaser, Thomas M.  
APPLICANT: Ito, Caryn Y.  
APPLICANT: Buckler, Alan J.  
APPLICANT: Pelletier, Jerry  
APPLICANT: Haber, Daniel A.  
APPLICANT: Rose, Elise A.  
APPLICANT: Housman, David E.  
APPLICANT: Brunsing, Wendy  
APPLICANT: Darveau, Andre  
TITLE OF INVENTION: Localization and Characterization of the  
TITLE OF INVENTION: Wilms' Tumor Gene  
FILE REFERENCE: 0050.1312-011  
CURRENT FILING DATE: 1998-03-09  
PRIOR APPLICATION NUMBER: US/09/037,179B  
PRIOR FILING DATE: 1993-08-02  
PRIOR APPLICATION NUMBER: US 07/614,161  
PRIOR FILING DATE: 1990-11-13  
PRIOR APPLICATION NUMBER: US 07/435,780  
PRIOR FILING DATE: 1989-11-13  
PRIOR APPLICATION NUMBER: US 07/795,323  
PRIOR FILING DATE: 1994-09-27  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 154  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-037-179B-5

Query Match 100.0%; Score 51; DB 4; Length 154;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
Db 40 RMFPNAPYL 48

## RESULT 3

US-08-234-783-2  
Sequence 2, Application US/08234783  
Patent No. 5622835  
GENERAL INFORMATION:  
APPLICANT: Herlyn, Meenhard  
APPLICANT: Morris, Jennifer  
APPLICANT: Rauscher III, Frank J.  
TITLE OF INVENTION: Wt1 Monoclonal Antibodies and Methods of  
TITLE OF INVENTION: Use Therefor  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr, PO Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/234,783  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: WST48USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 210 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-234-783-2

Query Match 100.0%; Score 51; DB 1; Length 210;  
Best Local Similarity 100.0%; Pred. No. 0.071;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
Db 137 RMFPNAPYL 145

## RESULT 4

US-08-456-907-2  
Sequence 2, Application US/08456907  
Patent No. 5633142  
GENERAL INFORMATION:  
APPLICANT: Herlyn, Meenhard  
APPLICANT: Morris, Jennifer  
APPLICANT: Rauscher III, Frank J.  
APPLICANT: Rodeck, Ulrich  
TITLE OF INVENTION: Wt1 Monoclonal Antibodies and Methods of  
TITLE OF INVENTION: Use Therefor  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr, PO Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/456,907  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/234,783  
FILING DATE: 28-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: WST48AUSA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:



LENGTH: 210 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-456-907-2

Query Match 100.0%; Score 51; DB 1; Length 210;  
Best Local Similarity 100.0%; Pred. No. 0.071;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 137 RMFPNAPYL 145

RESULT 5  
PCT-US95-05523-2  
Sequence 2, Application PC/TUS9505523

GENERAL INFORMATION:  
APPLICANT: The Wistar Institute of Anatomy and Biology  
TITLE OF INVENTION: WTI Monoclonal Antibodies and  
TITLE OF INVENTION: Methods of Use Therefor  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr, PO Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05523  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/234,783  
FILING DATE: 28-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: WST48PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 210 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-05523-2

Query Match 100.0%; Score 51; DB 5; Length 210;  
Best Local Similarity 100.0%; Pred. No. 0.071;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 137 RMFPNAPYL 145

RESULT 6  
US-08-102-942A-2  
Sequence 2, Application US/08102942A

GENERAL INFORMATION:  
APPLICANT: Call, Katherine M.  
APPLICANT: Glaeser, Thomas M.

APPLICANT: Ito, Caryn Y.  
APPLICANT: Buckler, Alan J.  
APPLICANT: Pelletier, Jerry  
APPLICANT: Haber, Daniel A.  
APPLICANT: Rose, Elise A.  
APPLICANT: Housman, David E.  
APPLICANT: Bruening, Wendy  
APPLICANT: Darveau, Andre  
TITLE OF INVENTION: Localization and Characterization of the  
TITLE OF INVENTION: Wilms' Tumor Gene  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/102,942A  
FILING DATE: 02-AUG-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: MIT-5194A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 345 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-102-942A-2

Query Match 100.0%; Score 51; DB 1; Length 345;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 42 RMFPNAPYL 50

RESULT 7  
US-09-037-179B-2  
Sequence 2, Application US/09037179B

GENERAL INFORMATION:  
APPLICANT: Call, Katherine M.  
APPLICANT: Glaeser, Thomas M.  
APPLICANT: Ito, Caryn Y.  
APPLICANT: Buckler, Alan J.  
APPLICANT: Pelletier, Jerry  
APPLICANT: Haber, Daniel A.  
APPLICANT: Rose, Elise A.  
APPLICANT: Housman, David E.  
APPLICANT: Bruening, Wendy  
APPLICANT: Darveau, Andre  
TITLE OF INVENTION: Localization and Characterization of the  
TITLE OF INVENTION: Wilms' Tumor Gene  
FILE REFERENCE: 0050,1312-011  
CURRENT APPLICATION NUMBER: US/09/037,179B  
CURRENT FILING DATE: 1998-03-09  
PRIOR APPLICATION NUMBER: US 08/102,942  
PRIOR FILING DATE: 1993-08-02

PRIOR APPLICATION NUMBER: US 07/614,161  
PRIOR FILING DATE: 1990-11-13  
PRIOR APPLICATION NUMBER: US 07/435,780  
PRIOR FILING DATE: 1989-11-13  
PRIOR APPLICATION NUMBER: US 07/795,323  
PRIOR FILING DATE: 1994-09-27  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-037-179B-2

Query Match 100.0%; Score 51; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
|||  
Db 42 RMFPNAPYL 50

RESULT 8  
US-08-234-783-4  
Sequence 4, Application US/08234783  
Patent No. 5622835  
GENERAL INFORMATION:  
APPLICANT: Herlyn, Meenhard  
APPLICANT: Morris, Jennifer  
APPLICANT: Rauscher III, Frank J.  
APPLICANT: Rodeck, Ulrich  
TITLE OF INVENTION: Wt1 Monoclonal Antibodies and Methods of  
TITLE OF INVENTION: Use Therefor  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESS: Howson and Howson  
STREET: Spring House Corporate Cntr, PO Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/234,783  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: WST48USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 429 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-234-783-4

Query Match 100.0%; Score 51; DB 1; Length 429;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
|||  
Db 126 RMFPNAPYL 134

RESULT 9  
US-08-456-907-4  
Sequence 4, Application US/08456907  
Patent No. 5633142  
GENERAL INFORMATION:  
APPLICANT: Herlyn, Meenhard  
APPLICANT: Morris, Jennifer  
APPLICANT: Rauscher III, Frank J.  
APPLICANT: Rodeck, Ulrich  
TITLE OF INVENTION: Wt1 Monoclonal Antibodies and Methods of  
TITLE OF INVENTION: Use Therefor  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESS: Howson and Howson  
STREET: Spring House Corporate Cntr, PO Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/456,907  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/234,783  
FILING DATE: 28-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: WST48USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 429 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-456-907-4

Query Match 100.0%; Score 51; DB 1; Length 429;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
|||  
Db 126 RMFPNAPYL 134

RESULT 10  
PCT-US95-05523-4  
Sequence 4, Application PC/TUS9505523  
GENERAL INFORMATION:  
APPLICANT: The Wistar Institute of Anatomy and Biology  
TITLE OF INVENTION: Wt1 Monoclonal Antibodies and  
TITLE OF INVENTION: Methods of Use Therefor  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESS: Howson and Howson  
STREET: Spring House Corporate Cntr, PO Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05523  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/234,783  
FILING DATE: 28-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 429 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-05523-4

Query Match 100.0%; Score 51; DB 5; Length 429;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 11  
US-08-102-942A-4  
Sequence 4, Application US/08102942A  
Patent No. 5726288  
GENERAL INFORMATION:  
APPLICANT: Call, Katherine M.  
APPLICANT: Glaser, Thomas M.  
APPLICANT: Ito, Caryn Y.  
APPLICANT: Buckler, Alan J.  
APPLICANT: Pelletier, Jerry  
APPLICANT: Haber, Daniel A.  
APPLICANT: Rose, Elise A.  
APPLICANT: Housman, David E.  
APPLICANT: Bruening, Wendy  
APPLICANT: Darveau, Andre  
TITLE OF INVENTION: Localization and Characterization of the  
NUMBER OF SEQUENCES: 8  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/102,942A  
FILING DATE: 02-AUG-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 449 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-102-942A-6

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 449 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-102-942A-4

Query Match 100.0%; Score 51; DB 1; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 12  
US-08-102-942A-6  
Sequence 6, Application US/08102942A  
Patent No. 5726288  
GENERAL INFORMATION:  
APPLICANT: Call, Katherine M.  
APPLICANT: Glaser, Thomas M.  
APPLICANT: Ito, Caryn Y.  
APPLICANT: Buckler, Alan J.  
APPLICANT: Pelletier, Jerry  
APPLICANT: Haber, Daniel A.  
APPLICANT: Rose, Elise A.  
APPLICANT: Housman, David E.  
APPLICANT: Bruening, Wendy  
APPLICANT: Darveau, Andre  
TITLE OF INVENTION: Localization and Characterization of the  
NUMBER OF SEQUENCES: 8  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/102,942A  
FILING DATE: 02-AUG-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 449 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-102-942A-6

OY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 13  
US-09-037-179B-4  
Sequence 4, Application US/09037179B  
Patent No. 6316599

GENERAL INFORMATION:  
APPLICANT: Call, Katherine M.  
APPLICANT: Glaser, Thomas M.  
APPLICANT: Ito, Caryn Y.  
APPLICANT: Buckler, Alan J.  
APPLICANT: Pelletier, Jerry  
APPLICANT: Haber, Daniel A.  
APPLICANT: Rose, Elise A.  
APPLICANT: Houseman, David E.  
APPLICANT: Bruening, Wendy

TITLE OF INVENTION: Localization and Characterization of the  
TITLE OF INVENTION: Wilms' Tumor Gene  
FILE REFERENCE: 0050.1312-011

CURRENT APPLICATION NUMBER: US/09/037,179B  
CURRENT FILING DATE: 1998-03-09  
PRIOR APPLICATION NUMBER: US 08/102,942  
PRIOR FILING DATE: 1993-08-02

PRIOR APPLICATION NUMBER: US 07/614,161  
PRIOR FILING DATE: 1990-11-13

PRIOR APPLICATION NUMBER: US 07/435,780  
PRIOR FILING DATE: 1989-11-13

PRIOR APPLICATION NUMBER: US 07/795,323  
PRIOR FILING DATE: 1994-09-27

NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4  
LENGTH: 449

TYPE: PRT

ORGANISM: Unknown

FEATURE:  
OTHER INFORMATION: Murine

US-09-037-179B-4

Query Match 100.0%; Score 51; DB 4; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 14  
US-09-037-179B-6  
Sequence 6, Application US/09037179B  
Patent No. 6316599

GENERAL INFORMATION:  
APPLICANT: Call, Katherine M.  
APPLICANT: Glaser, Thomas M.  
APPLICANT: Ito, Caryn Y.  
APPLICANT: Buckler, Alan J.  
APPLICANT: Pelletier, Jerry  
APPLICANT: Haber, Daniel A.  
APPLICANT: Rose, Elise A.  
APPLICANT: Houseman, David E.  
APPLICANT: Bruening, Wendy

TITLE OF INVENTION: Localization and Characterization of the  
TITLE OF INVENTION: Wilms' Tumor Gene  
FILE REFERENCE: 0050.1312-011

CURRENT APPLICATION NUMBER: US/09/037,179B  
CURRENT FILING DATE: 1998-03-09

PRIOR APPLICATION NUMBER: US 08/102,942  
PRIOR FILING DATE: 1993-08-02  
PRIOR APPLICATION NUMBER: US 07/614,161  
PRIOR FILING DATE: 1990-11-13  
PRIOR APPLICATION NUMBER: US 07/435,780  
PRIOR FILING DATE: 1989-11-13  
PRIOR APPLICATION NUMBER: US 07/795,323  
PRIOR FILING DATE: 1994-09-27  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Homo sapien

US-09-037-179B-6

Query Match 100.0%; Score 51; DB 4; Length 449;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
Db 126 RMFPNAPYL 134

RESULT 15  
US-09-252-991A-19580  
Sequence 19580, Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 19580

LENGTH: 269

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-19580

Query Match 74.5%; Score 38; DB 4; Length 269;  
Best Local Similarity 75.0%; Pred. No. 19;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MFPPAPYL 9  
Db 139 MFPPAPYL 146

Search completed: January 21, 2004, 08:45:42  
Job time : 23 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 21, 2004, 08:49:30 ; Search time 20 Seconds  
(without alignments)  
43.276 Million cell updates/sec

Title: US-09-625-963A-1  
Perfect score: 51  
Sequence: 1 RMFPNAPYL 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 263308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 789

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*

1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	37.3	9	2	S70345
2	18	35.3	9	2	D48186
3	17	33.3	9	2	PH1408
4	17	33.3	9	2	JS0302
5	17	33.3	9	2	A60320
6	17	33.3	9	2	PI0139
7	16	31.4	9	2	S21230
8	16	31.4	9	2	S21230
9	16	31.4	9	2	A44787
10	16	31.4	9	2	D41978
11	15	29.4	6	4	S15596
12	15	29.4	9	2	S66607
13	15	29.4	9	2	A61620
14	15	29.4	9	2	PH1591
15	14	27.5	5	2	JS0319
16	14	27.5	8	2	S21288
17	14	27.5	8	2	PT0030
18	14	27.5	8	2	D47393
19	14	27.5	8	2	B47393
20	14	27.5	8	2	B45800
21	14	27.5	8	4	I54017
22	14	27.5	9	2	S66419
23	14	27.5	9	2	S70332
24	14	27.5	9	2	A29477
25	14	27.5	9	2	S39766
26	14	27.5	9	2	S77984
27	14	27.5	9	2	S66635
28	14	27.5	9	2	S10784
29	13	25.5	4	2	S53508

30	13	25.5	6	2	A61049	halo-toxin - Pseud
31	13	25.5	6	2	A44916	mesquitocidal toxin
32	13	25.5	7	2	A15398	choline oxidase (E
33	13	25.5	7	2	I50210	gene c-rel protein
34	13	25.5	7	2	B48394	glycoprotein compo
35	13	25.5	8	2	S08995	hypertrehalosemic
36	13	25.5	8	2	S08996	hypertrehalosemic
37	13	25.5	8	2	A49823	adipokineic hormo
38	13	25.5	8	2	B49823	adipokineic hormo
39	13	25.5	8	2	A44960	neuropeptide Led-C
40	13	25.5	8	2	B44960	neuropeptide Led-C
41	13	25.5	8	2	A43976	hypertrehalosemic
42	13	25.5	8	2	B43976	hypertrehalosemic
43	13	25.5	8	2	PH1407	Ig heavy chain V r
44	13	25.5	8	2	PH1407	capsid protein VP-
45	13	25.5	8	2	B39745	endoglycosylcerami

## ALIGNMENTS

## RESULT 1

amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragments)  
C:Species: Aspergillus niger  
C:Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998  
C:Accession: S70345  
R:Frederic, I.; Pec, P.; Luhova, L.; Toyama, H.; Matsushita, K.; Hirota, S.; Kitagawa, T.  
Biochim. Biophys. Acta 1295, 59-72, 1996  
A:Title: Two amine oxidases from Aspergillus niger AKU 3302 contain topa quinone as the  
A:Reference number: S70344; MUID:96283794; PMID:8679675  
A:Accession: S70345  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5;6-9<FR>  
C:Keywords: oxidoreductase

## Query Match

Best local similarity 37.3%; Score 19; DB 2; Length 9;  
Matches 3; Conservative 0; Mismatches 2; Indels 0;

QY 4 PNAPY 8  
DB 5 PNKEY 9

## RESULT 2

ATPase R1 subunit - wood tobacco (fragment)  
D48186  
C:Species: Nicotiana glauca (wood tobacco)  
C:Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Feb-1997  
C:Accession: D48186  
R:De Paape, R.; Forchioni, A.; Chetrit, P.; Vedel, F.  
Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5938, 1993  
A:Title: Specific mitochondrial proteins in pollen: presence of an additional ATP synthase  
A:Reference number: A48186; MUID:93317598; PMID:8327463  
A:Accession: D48186  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9<DEL>  
A:Experimental source: pollen  
A>Note: sequence extracted from NCBI backbone (NCBI:P:134871)

## Query Match

Best local similarity 35.3%; Score 18; DB 2; Length 9;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 APY 8  
DB 6 APY 8

## RESULT 3

PH1408  
Ig heavy chain V region - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
C/Accession: PH1408; PH1405  
R/Shirasawa, T.; Miyazoe, T.; Hagihara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Teraoka, Y.; Exp. Med. 176, 1209-1214, 1992  
A/Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in 1a virus.  
A/Reference number: PH1403; MUID:93018837; PMID:1402663  
A/Accession: PH1408  
A/Molecule type: DNA  
A/Residues: 1-7 <SH1>  
A/Experimental source: clone micro m+ 46-12-2  
A/Accession: PH1405  
A/Molecule type: DNA  
A/Residues: 1-7 <SH12>  
A/Experimental source: clone micro m+ 46-6  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 17; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RMPF 4  
| | | |  
Db 4 RRP 7

#### RESULT 4

US0302 xenopsin-related peptide 2 - turkey  
N/Contains: xenopsin-related peptide 1  
C/Species: Meleagris gallopavo (common turkey)  
C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 18-Aug-2000  
C/Accession: JS0302  
R/Carraway, R.E.; Cochran, D.E.; Mitra, S.P.  
Regul. Pept. 22, 303-314, 1988  
A/Title: Xenopsin-related peptide generated in avian gastric extracts.  
A/Reference number: JS0302; MUID:89042995; PMID:2460902  
A/Accession: JS0302

A/Molecule type: protein  
A/Residues: 1-9 <CAR>  
C/Comment: The peptides are present within several tissues primarily in large molecular C/Superfamily: yeast coatomer complex alpha chain; WD repeat homology  
C/Keywords: neuropeptide  
F/1-9/Product: xenopsin-related peptide 2 #status experimental <XP2>  
F/2-9/Product: xenopsin-related peptide 1 #status experimental <XP1>

Query Match 33.3%; Score 17; DB 2; Length 9;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNPYL 9  
| | | |  
Db 3 PKRPWI 8

#### RESULT 5

A60320 xenopsin-related peptide 2 - rat  
N/Contains: xenopsin-related peptide 1  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 18-Aug-2000  
C/Accession: A60320  
R/Carraway, R.E.; Mitra, S.P.; Muraki, K.  
Regul. Pept. 29, 229-239, 1990  
A/Title: Isolation and structures of xenopsin-related peptides from rat stomach, liver &

A/Reference number: A60320; MUID:91018491; PMID:2217904  
A/Accession: A60320  
A/Molecule type: protein  
A/Residues: 1-9 <CAR>

A/Note: the authors purified these peptides from pepsin-treated extracts of stomach, liver & C/Comment: Xenopsin and xenopsin-related peptides are similar to neurotensin in sequence C/Superfamily: yeast coatomer complex alpha chain; WD repeat homology  
C/Keywords: neuropeptide  
F/1-9/Product: xenopsin-related peptide 2 #status experimental <MAT1>  
F/2-9/Product: xenopsin-related peptide 1 #status experimental <MAT2>

Query Match 33.3%; Score 17; DB 2; Length 9;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNPYL 9  
| | | |  
Db 3 PKRPWI 8

#### RESULT 6

PL0139 carbon-monoxide dehydrogenase (BC 1.2.99.2) large chain - Pseudomonas carboxydoflava (fr C/Species: Pseudomonas carboxydoflava  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 28-Apr-1993  
C/Accession: PL0139  
R/Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.  
Arch. Microbiol. 152, 335-341, 1989  
A/Title: Homology and distribution of CO dehydrogenase structural genes in carboxydofl A/Reference number: PL0138; MUID:90055678; PMID:2818128  
A/Accession: PL0139

A/Molecule type: protein  
A/Residues: 1-9 <KRA>  
A/Note: 2-Met is also found  
C/Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me C/Keywords: oxidoreductase

Query Match 33.3%; Score 17; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 NMP 7  
| | | |  
Db 2 NMP 4

#### RESULT 7

S21230 dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)  
C/Species: Phyllomedusa bicolor (two-colored leaf frog)  
C/Date: 19-Mar-1997 #sequence\_revision 10-Oct-1997 #text\_change 18-Aug-2000  
C/Accession: S21230  
R/Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G. FEBS Lett. 302, 151-154, 1992  
A/Title: Identification and characterization of two dermorphins from skin extracts of th A/Reference number: S21152; MUID:92339502; PMID:1633846  
A/Accession: S21230

A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-7 <MTG>  
C/Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 31.4%; Score 16; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 FPN 5  
| | | |  
Db 5 FPN 7

#### RESULT 8

I57018 gene cfr protein - mouse (fragment)  
C/Species: Mus sp. (mouse)  
C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 28-Feb-1997  
C/Accession: I57018

R:Dorin, J.R.; Stevenson, B.J.; Fleming, S.; Alton, E.W.; Dickinson, P.; Porteous, D.J.  
 Mamm. Genome 5, 465-472, 1994  
 A>Title: Long-term survival of the exon 10 insertional cystic fibrosis mutant mouse is a  
 A:Reference number: 157018; MUID:95037043; PMID:7949729  
 A:Accession: 157018  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-8 <RSS>  
 A:Cross-references: GB:S74246; MUID:9710482  
 A:Accession: A44787  
 A:Gene: Cftr

Query Match 31.4%; Score 16; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 PNPYL 9  
 |||  
 Db 2 PNDPM 7

RESULT 9  
 A44787  
 calliFMRamide 10 - bluebottle fly (Calliphora vomitoria)  
 C:Species: Calliphora vomitoria  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Mar-1999  
 C:Accession: A44787  
 R:Dive, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992  
 A>Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desl  
 A:Reference number: A41978; MUID:92196111; PMID:1549595  
 A:Accession: A44787  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9 <DUV>  
 C:Keywords: amidated carboxyl end; neuropeptide  
 F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 31.4%; Score 16; DB 2; Length 9;  
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNPYL 9  
 |||  
 Db 2 PNDPM 7

RESULT 10  
 D41978  
 calliFMRamide 4 - bluebottle fly (Calliphora vomitoria)  
 C:Species: Calliphora vomitoria  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Mar-1999  
 C:Accession: D41978  
 R:Dive, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992  
 A>Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desl  
 A:Reference number: A41978; MUID:92196111; PMID:1549595  
 A:Accession: D41978  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9 <DUV>  
 C:Keywords: amidated carboxyl end; neuropeptide  
 F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 31.4%; Score 16; DB 2; Length 9;  
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNPYL 9  
 |||  
 Db 2 PNDPM 7

RESULT 11  
 S15596  
 orf3 rara 5'-region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 04-Jun-1999 #sequence\_revision 04-Jun-1999 #text\_change 28-Jun-1999  
 C:Accession: S15596  
 R:Brand, N.J.; Peckovich, M.; Chambon, P.  
 Nucleic Acids Res. 18, 6799-6806, 1990  
 A>Title: Characterization of a functional promoter for the human retinoic acid receptor-  
 A:Reference number: S15594; MUID:91086249; PMID:2175878  
 A:Accession: S15596  
 A:Molecule type: DNA  
 A:Residues: 1-6 <BBA>  
 A:Cross-references: EMBL:X56058; MUID:935876  
 A>Note: this ORF from Fig. 2 is not annotated in GenBank entry HSRAR2, release 111.0  
 C:Comment: This sequence is not thought to be translated.  
 C:Genetics:  
 A:Gene: GDB:RARA  
 A:Cross-references: GDB:120337; OMIM:180240  
 A:Map position: 17q12-17q12

Query Match 29.4%; Score 15; DB 4; Length 6;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MFNNA 6  
 |||  
 Db 1 MAPSA 5

RESULT 12  
 S66607  
 quinoline 2-oxidoreductase beta chain - Comamonas testosteroni (fragment)  
 C:Species: Comamonas testosteroni  
 C>Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
 C:Accession: S66607  
 R:Schach, S.; Tshisuka, B.; Felzner, S.; Lings, F.  
 Eur. J. Biochem. 232, 535-544, 1995  
 A>Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from  
 A:Reference number: S66606; MUID:96035889; PMID:7556204  
 A:Accession: S66607  
 A:Molecule type: protein  
 A:Residues: 1-9 <SCH>  
 A:Experimental source: strain 63

Query Match 29.4%; Score 15; DB 2; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 FPNAPY 8  
 |||  
 Db 3 FPARAY 8

RESULT 13  
 A61620  
 locustamyotropin III - migratory locust  
 C:Species: Locusta migratoria (migratory locust)  
 C>Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 11-Jul-1997  
 C:Accession: A61620  
 R:Schroofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.  
 Insect Biochem. Mol. Biol. 22, 447-452, 1992  
 A>Title: Isolation, identification and synthesis of locustamyotropin III and IV, two add  
 A:Reference number: A61620  
 A:Accession: A61620  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9 <SCH>  
 C:Keywords: amidated carboxyl end; neuropeptide  
 F:9/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 29.4%; Score 15; DB 2; Length 9;  
 Best Local Similarity 44.4%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9  
 Db 1 RQPFVFPRL 9

## RESULT 14

PH1591  
 Ig H chain V-D-J region (wild-type clone 142) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C:Accession: PH1591  
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
 A:Reference number: PH1580; MID:93301609; PMID:8315387  
 A:Accession: PH1591  
 A:Molecule type: DNA  
 A:Residues: 1-9 <LEV>  
 A:Experimental source: bone marrow pre-B lymphocyte  
 C:Keywords: immunoglobulin

Query Match 29.4%; Score 15; DB 2; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 APY 8  
 Db 5 SPY 7

## RESULT 15

JS0319  
 subesophageal ganglion pentapeptide - house cricket  
 C:Species: Acheta domesticus (house cricket)  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C:Accession: JS0319  
 R:Wicker, C.; Wicker, C.  
 Comp. Biochem. Physiol. C 88, 185-187, 1987  
 A:Title: Isolation and structure of a peptide isolated from the subesophageal ganglion  
 A:Reference number: JS0319  
 A:Accession: JS0319  
 A:Molecule type: protein  
 A:Residues: 1-5 <WIC>

Query Match 27.5%; Score 14; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 APY 8  
 Db 3 APF 5

Search completed: January 21, 2004, 08:52:50  
 Job time : 22 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 21, 2004, 08:45:45 ; Search time 11 Seconds  
(without alignments)  
38.476 Million cell updates/sec

Title: US-09-625-963A-1  
Sequence: 1 MFPPNAPYL 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 251

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	22	43.1	9 1 UPA7_HUMAN	P30093 homo sapien
2	18	35.3	7 1 GFRP_MOUSE	P90925 mus musculu
3	18	35.3	7 1 UN06_PIRNS	P81675 pinus pinas
4	18	35.3	8 1 B44K_PORGI	P81886 porphyromon
5	17	33.3	8 1 PPK2_PERAM	P82692 periplaneta
6	17	33.3	9 1 OXYF_SCYCA	P42997 scylliorhinu
7	17	33.3	9 1 OXYF_OCTVU	P80027 octopus vul
8	16	31.4	9 1 PAR4_CALVO	P41859 calliphora
9	16	31.4	9 1 PAR4_CALVO	P41865 calliphora
10	16	31.4	9 1 FLA2_TREAY	P80159 treponema h
11	16	31.4	9 1 UPA3_HUMAN	P30089 homo sapien
12	15	29.4	8 1 AL17_CARMA	P81809 carcius ma
13	15	29.4	9 1 LMT3_LOCM1	P41489 locusta mig
14	14	27.5	5 1 SUGA_ACHDO	P19991 acheta dome
15	14	27.5	7 1 ALL3_CARMA	P81806 carcius ma
16	14	27.5	7 1 ALL4_CARMA	P81807 carcius ma
17	14	27.5	7 1 ALL5_CARMA	P81808 carcius ma
18	14	27.5	7 1 FARI_HELT	P41871 helisoma tr
19	14	27.5	8 1 AL15_CARMA	P81818 carcius ma
20	14	27.5	8 1 AL16_CARMA	P81819 carcius ma
21	14	27.5	8 1 AL13_CYPDO	P82154 cydia pomon
22	14	27.5	8 1 ALL4_CALVO	P41840 calliphora
23	14	27.5	8 1 ALL4_CYPDO	P82155 cydia pomon
24	14	27.5	8 1 ALL5_CALVO	P41841 calliphora
25	14	27.5	8 1 ALL8_CARMA	P81811 carcius ma
26	14	27.5	8 1 ALL9_CARMA	P81812 carcius ma
27	14	27.5	8 1 FUS3_FUSCO	P81010 fusarium so
28	14	27.5	9 1 AL10_CARMA	P81813 carcius ma
29	14	27.5	9 1 COXE_THOOS	P80975 thunnus obe
30	14	27.5	9 1 DNFI_LOCM1	P16339 locusta mig
31	14	27.5	9 1 NEUX_HUMAN	P04277 homo sapien
32	14	27.5	9 1 TKCI_CALVO	P41517 calliphora
33	13	25.5	5 1 PAP2_PANWA	P81864 pardachirus

34	13	25.5	7 1 CHO3_ALCSP	P16101 alcaligenes
35	13	25.5	7 1 PAR4_PANRE	P41875 panagrellus
36	13	25.5	7 1 MNPI_LEPDE	P42984 lepicinotars
37	13	25.5	7 1 UF04_MOUSE	P38642 mus musculu
38	13	25.5	8 1 FARI_PANRE	P41872 panagrellus
39	13	25.5	8 1 PAR4_MACRS	P83277 macrobrachi
40	13	25.5	8 1 HTF1_PERAM	P04548 periplaneta
41	13	25.5	8 1 HTF2_PERAM	P04549 periplaneta
42	13	25.5	8 1 HTP1_TENMO	P25419 tenobrio mo
43	13	25.5	8 1 PPK3_PERAM	P82618 periplaneta
44	13	25.5	8 1 UF06_MOUSE	P38644 mus musculu
45	13	25.5	8 1 UPA1_HUMAN	P30087 homo sapien

## ALIGNMENTS

RESULT 1  
ID UPA7\_HUMAN STANDARD; PRT; 9 AA.  
AC P30093;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 18) (Fragment).  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing."  
RL Electrophoresis 13:707-714 (1992).  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 5.05, ITS MW IS: 37 KDa.  
DR SWISS-2DPAGE; P30093; HUMAN.  
FT NON TER 1  
FT UNSURE 5  
FT NON TER 9  
SQ SEQUENCE 9 AA; 1042 MW; 5C14477AEB072C7 CRC64;  
Query Match 43.1%; Score 22; DB 1; Length 9;  
Best Local Similarity 42.9%; Pred. No. 1.3e+05;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2 MFPPNAPYL 8  
DB 2 LVPEXPY 8  
RESULT 2  
ID GFRP\_MOUSE STANDARD; PRT; 7 AA.  
AC P90925;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE GFR cyclonhydrolase I feedback regulatory protein (P35) (Fragment).  
GN GCFR OR GFRP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Liver;  
RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,  
RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,

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RA Cowthorne M.;
RT Submitted (Aug-1998) to the SWISS-PROT data bank.
RL -1- FUNCTION: MEDIATES TETRAHYDROBIOTERIN INHIBITION OF GTP
CC CYCLOHYDROLASE 1. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
CC (BY SIMILARITY).
CC -1- SUBUNIT: Homodimer (By similarity).
CC SWISS-2DPAGE: P99025; MOUSE.
FT INIT MET 0
FT NON TER 0
SQ SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;

Query Match
Best Local Similarity 35.3%; Score 18; DB 1; Length 7;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PYL 9
DB 1 PYL 3

RESULT 3
ID UN06 PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Pinus.
NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costra P., Pionneau C., Bauw G., Dubos C., Bahrmann N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins."
CC Electrophoresis 20:1098-1108(1999).
RL -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS 6.6, ITS MW IS: 25 Kda.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match
Best Local Similarity 35.3%; Score 18; DB 1; Length 7;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 MFPNAPY 8
DB 1 LYGNLPF 7

RESULT 4
ID B44K_PORGI STANDARD; PRT; 8 AA.
AC P81886;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 44 kDa immunogenic protein (Fragment).
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
NCBI_TaxID=837;
RN [1]
RP SEQUENCE.
RC STRAIN=VPB 3492;
RX MEDLINE=20198497; PubMed=10731616;
RA Norris J.M., Love D.N.;

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RT "Serum antibody responses of cats to soluble whole cell antigens of
RT feline Porphyromonas gingivalis."
RL Vet. Microbiol. 73:37-49(2000).
CC -1- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
CC Antigen.
FT NON TER 8
FT NON TER 8
SQ SEQUENCE 8 AA; 989 MW; 9554540326CB476D CRC64;

Query Match
Best Local Similarity 35.3%; Score 18; DB 1; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 APY 8
DB 1 APY 3

RESULT 5
ID PK2_PERAM STANDARD; PRT; 8 AA.
AC P82692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RT retrocerebral complex of the American cockroach."
RL Peptides 18:473-476(1997).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach."
RL J. Comp. Neurol. 419:352-363(2000).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -1- MASS SPECTROMETRY: MM=883; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro: IPR001484; Pyrokinin.
DR PROSITE: PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 8
FT MOD RES 8
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match
Best Local Similarity 33.3%; Score 17; DB 1; Length 8;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNAPYL 9
DB 3 PFAFRL 8

RESULT 6
ID OXYF_SCYCA STANDARD; PRT; 9 AA.
AC P42957;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Phasvatocin.

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OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphi; Galeoidea; Garcharhiniformes;  
 OC Scyliorhinidae; Scyliorhinus.  
 OX NCBI\_TaxID=7830;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pituitary; PubMed=7972045;  
 RX MEDLINE=95062247;  
 RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;  
 RT "Special evolution of neurohypophysial hormones in cartilaginous  
 fishes: asatocin and phasatocin, two oxytocin-like peptides  
 isolated from the spotted dogfish (Scyliorhinus canicula)." ;  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).  
 CC -1- SIMILARITY: DISPLAYS OXYTOCIN ACTIVITY ON RAT UTERUS.  
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR InterPro; IPR000981; Neurhyp\_horm.  
 DR Pfam; PF00220; hormone4; 1.  
 DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KM Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD\_RES 9 9  
 FT SEQUENCE 9 AA; 1016 MW; 17EDD76B44449DB CRC64;  
 SQ  
 Query Match 33.3%; Score 17; DB 1; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 PNPAP 7  
 DB 3 PNPAP 7

RESULT 7  
 OXYT OCTVU STANDARD; PRT; 9 AA.  
 ID OXYT OCTVU  
 AC P80027;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Cephalotocin.  
 OS Octopus vulgaris (Octopus).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Octopodiformes; Octopoda; Incurtata; Octopodidae; Octopus.  
 OX NCBI\_TaxID=6645;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Nerve endings;  
 RX MEDLINE=92270139; PubMed=1589145;  
 RA Reich G.;  
 RT "A new peptide of the oxytocin/vasopressin family isolated from  
 nerves of the cephalopod Octopus vulgaris." ;  
 RL Neurosci. Lett. 134:191-194(1992).  
 CC -1- FUNCTION: HAS A ROLE IN THE NEUROSECRETORY SYSTEM OF THE VENA  
 CAVA.  
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR InterPro; IPR000981; Neurhyp\_horm.  
 DR Pfam; PF00220; hormone4; 1.  
 DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KM Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD\_RES 9 9  
 FT SEQUENCE 9 AA; 1072 MW; 17FF476B45409DB CRC64;  
 SQ

Query Match 33.3%; Score 17; DB 1; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 PNPAP 7  
 DB 3 PNPAP 7

RESULT 8  
 FARA CALVO STANDARD; PRT; 9 AA.  
 ID FARA CALVO  
 AC P4185;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Calliphrasamide 4.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Thoracic ganglion;  
 RX MEDLINE=92196111; PubMed=1549595;  
 RA Dve H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.;  
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 neuropeptides (designated calliphrasamides) from the blowfly  
 Calliphora vomitoria." ;  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 DR PIR; D41978; D41978.  
 DR Neuropeptide; Amidation.  
 FT MOD\_RES 9 9  
 FT SEQUENCE 9 AA; 1182 MW; 31730699CAB6D457 CRC64;  
 SQ

Query Match 31.4%; Score 16; DB 1; Length 9;  
 Best Local Similarity 33.3%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNPAP 9  
 DB 2 PNPAP 7

RESULT 9  
 FARA CALVO STANDARD; PRT; 9 AA.  
 ID FARA CALVO  
 AC P4185;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Calliphrasamide 10.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Thoracic ganglion;  
 RX MEDLINE=92196111; PubMed=1549595;  
 RA Dve H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.;  
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 neuropeptides (designated calliphrasamides) from the blowfly  
 Calliphora vomitoria." ;  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 DR PIR; A44787; A44787.  
 DR Neuropeptide; Amidation.  
 FT MOD\_RES 9 9  
 FT UNSTORE 1 1  
 FT SEQUENCE 9 AA; 1183 MW; 29D00699CAB40457 CRC64;  
 SQ

Query Match 31.4%; Score 16; DB 1; Length 9;  
 Best Local Similarity 33.3%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNPAPL 9  
DB 2 PNRDFM 7

## RESULT 10

FLA2\_TREHY STANDARD; PRT; 9 AA.  
ID FLA2\_TREHY  
AC P80159;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Flagellar filament outer layer protein flaa2 (35 kDa sheath protein) (Fragment).  
GN FLA2.  
OS Treponema hyodysenteriae (Serpulina hyodysenteriae).  
OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspirae.  
OX NCBI\_TaxID=159;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=C5;  
RX MEDLINE=93139764; PubMed=1487733;  
RA Koopman M.B.H., Baets F., Van Vorstenbosch C.J.A.H.V.,  
RA van der Zelft B.A.M., Kusters J.G.;  
RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are composed of two sheath proteins and three core proteins."  
RL J. Gen. Microbiol. 138:2697-2706(1992).  
CC -1- FUNCTION: COMPONENT OF THE OUTER LAYER OF THE FLAGELLA.  
CC -1- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO SHEATH PROTEINS, FLA1 (44 kDa) AND FLA2 (35 kDa) AROUND A CORE THAT CONTAINS THREE PROTEINS FLA1 (37 kDa), FLA2 (34 kDa) AND FLA3 (32 kDa).  
CC -1- SUBCELLULAR LOCATION: Periplasmic flagellum.  
KW Flagella; Periplasmic.  
FT UNSURE 2  
FT UNSURE 2  
FT NON TER 8 9  
FT NON TER 9 9  
SQ SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;  
Query Match 31.4%; Score 16; DB 1; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1.3e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 MFPN 5  
DB 6 MFEN 9

RESULT 11  
UPA3\_HUMAN STANDARD; PRT; 9 AA.  
ID UPA3\_HUMAN  
AC P30089;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C., Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B., Hochstrasser D.F.;  
RA "Plasma protein map: an update by microsequencing."  
RL "Electrophoresis 13:707-714(1992).  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 4.6, ITS MW IS: 46 kDa.  
DR SWISS-2DPAGE; P30089; HUMAN.

FT NON TER 1 1  
FT NON TER 9 9  
SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;  
Query Match 31.4%; Score 16; DB 1; Length 9;  
Best Local Similarity 28.6%; Pred. No. 1.3e+05;  
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 MFPNAPY 8  
DB 3 LFPXTDF 9

## RESULT 12

ALL7\_CARMA STANDARD; PRT; 8 AA.  
ID ALL7\_CARMA  
AC P81809; P81804; P81810;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Carcinustatin 7 [Contains: Carcinustatin 6; Carcinustatin 1].  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=96121193; PubMed=9461295;  
RA Dye H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas."  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation; Multigene family.  
FT PEPTIDE 1 8  
FT PEPTIDE 2 8  
FT PEPTIDE 4 8  
FT MOD RES 8 8  
SQ SEQUENCE 8 AA; 825 MW; 922879CDBC4775BD CRC64;  
Query Match 29.4%; Score 15; DB 1; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 APY 8  
DB 2 SPY 4

RESULT 13  
LMT3\_LOCOMI STANDARD; PRT; 9 AA.  
ID LMT3\_LOCOMI  
AC P41489;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Locustamyotropin 3 (LOM-MT-3).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygora;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Brain;  
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P., de Loof A.;  
RA "Isolation, identification and synthesis of locustamyotropin III and IV, two additional neuropeptides of Locusta migratoria: members of the

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RT locustamycotropin peptide family."
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -1- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
CC PIR: A61620; A61620.
DR InterPro: IPR001484; Pyrokinin.
DR PROSITE: PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1140 MW; DSAE1772C9D776C6 CRC64;

Query Match 29.4%; Score 15; DB 1; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9
DB 1 RQQPFVPRLL 9

RESULT 14
SUGA_ACHDO STANDARD; PRT; 5 AA.
ID SUGA_ACHDO
AC P19931.
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DS Suboesophageal ganglion pentapeptide.
DS Achneta domesticus (House cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Achneta.
OX NCBI_TaxID=6997;
RN [1]
RP SEQUENCE.
RA Wicker C., Wicker C.;
RT "Isolation and structure of a peptide isolated from the
RT suboesophageal ganglion of Achneta domesticus (Orthoptera).";
RL Comp. Biochem. Physiol. 88C:185-187(1987).
CC -1- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL
CC GANGLIA.
CC PIR: JS0319; JS0319.
DR PIR: JS0319; JS0319.
SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;

Query Match 27.5%; Score 14; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 APY 8
DB 3 APF 5

RESULT 15
ALL3_CARMA STANDARD; PRT; 7 AA.
ID ALL3_CARMA
AC P81806;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 3. (Common shore crab) (Green crab).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;

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RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Multigene family.
SQ SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;

Query Match 27.5%; Score 14; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PY 8
DB 2 PY 3

Search completed: January 21, 2004, 08:51:29
Job time : 13 secs

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: January 21, 2004, 08:48:55 ; Search time 34 Seconds  
(without alignments)  
68.308 Million cell updates/sec

Title: US-09-625-963A-1

Perfect score: 51

Sequence: 1 RMEPNAPYL 9

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 775

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriopl:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	39.2	9	4 Q9UMF3	Q9UMF3 homo sapien
2	17	33.3	8	4 Q9UJ50	Q9UJ50 homo sapien
3	17	33.3	9	4 Q96T78	Q96T78 homo sapien
4	17	33.3	9	10 P82429	P82429 nicotiana t
5	16	31.4	8	2 Q9RT72	Q9RT72 escherichia
6	16	31.4	8	3 Q9P8E5	Q9P8E5 kuuyveromyc
7	15	29.4	8	5 Q9TWH6	Q9TWH6 periteneis
8	9	29.4	8	10 Q8GTG5	Q8GTG5 lycopersico
9	15	29.4	9	4 Q9UCS8	Q9UCS8 homo sapien
10	15	29.4	9	4 Q9H522	Q9H522 homo sapien
11	15	29.4	9	10 Q9S8U8	Q9S8U8 oryza sativ
12	15	27.5	7	8 Q98866	Q98866 spinacia ol
13	14	27.5	7	15 Q07624	Q07624 rous sarcom
14	14	27.5	8	3 P82858	P82858 puccinia re
15	14	27.5	8	8 Q8W8G2	Q8W8G2 diadema sav
16	14	27.5	8	8 Q8W8G4	Q8W8G4 diadema mex

17	14	27.5	8	8 Q8W8G5	Q8W8G5 diadema ant
18	14	27.5	8	8 Q8W8G3	Q8W8G3 diadema pau
19	14	27.5	8	8 Q8W8P5	Q8W8P5 diadema pau
20	14	27.5	8	11 Q8K3Z7	Q8K3Z7 mus musculus
21	14	27.5	8	11 Q99P40	Q99P40 mus musculus
22	14	27.5	9	2 P83157	P83157 anabaena sp
23	14	27.5	9	6 Q9TRU7	Q9TRU7 bos taurus
24	14	27.5	9	8 Q8WFS4	Q8WFS4 diadema mex
25	14	27.5	9	8 Q8W8X4	Q8W8X4 diadema mex
26	14	27.5	9	8 Q9T2K9	Q9T2K9 spinacia ol
27	14	27.5	9	8 Q8W8W5	Q8W8W5 diadema set
28	14	27.5	9	8 Q8W8W6	Q8W8W6 diadema ant
29	14	27.5	9	12 Q67605	Q67605 squash leaf
30	14	27.5	9	12 Q67606	Q67606 squash leaf
31	13	25.5	8	2 Q9AGP4	Q9AGP4 arthrobaacte
32	13	25.5	8	2 Q49534	Q49534 mycoplasma
33	13	25.5	9	2 Q99193	Q99193 pseudomonas
34	13	25.5	9	4 Q9UKJ6	Q9UKJ6 homo sapien
35	13	25.5	9	4 Q9UC36	Q9UC36 homo sapien
36	13	25.5	9	6 Q28121	Q28121 bos taurus
37	13	25.5	9	12 Q71066	Q71066 canine diat
38	13	25.5	9	16 Q935G1	Q935G1 salmonella
39	12	23.5	8	4 Q9P0K3	Q9P0K3 homo sapien
40	12	23.5	8	10 P82324	P82324 pisum sativ
41	12	23.5	8	11 Q9JID7	Q9JID7 mesocricetu
42	12	23.5	8	11 P82598	P82598 rattus norv
43	12	23.5	8	12 Q9WJ33	Q9WJ33 pseudorabie
44	12	23.5	8	12 Q90345	Q90345 hepaticis g
45	12	23.5	8	13 Q8JFN8	Q8JFN8 gallus gall

#### ALIGNMENTS

RESULT 1					
Q9UMF3	Q9UMF3	PRELIMINARY;	PRT;	9 AA.	
AC	Q9UMF3;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)				
DE	PD-1 protein (Fragment).				
GN	PD-1				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE=97473511; PubMed=9332365;				
RA	Finger L.R., Pu J., Wasserman R., Vibhakar R., Louie E., Hardy R.R.,				
RA	Burrows P.D., Billips L.G.;				
RT	"The human PD-1 gene: complete cDNA, genomic organization, and				
RT	developmentally regulated expression in B cell progenitors.";				
RL	Gene 197177-187(1997).				
DR	EMBL, U64864; AAC51774.1; ..				
FT	NON TER				
FT	SEQUENCE 9 AA; 1067 MW; DD4A676DC6C76046 CRC64;				
SQ					
Query Match					
Best Local Similarity 39.2%; Score 20; DB 4; Length 9;					
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;					
QY	4 PNPAY 8				
Db	4 PNPAY 8				
RESULT 2					
Q9UJ50	Q9UJ50	PRELIMINARY;	PRT;	8 AA.	
AC	Q9UJ50;				

DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Lactophilin-2 (Fragment).  
 GN LPHH1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxId=9606;  
 RX MEDLINE=99153747; PubMed=10030676;  
 RA White G.R.M., Varley J.M., Heighway J.;  
 RT "Isolation and characterisation of a human homologue of the  
 RT lactophilin gene from a region of 1p31.1 implicated in breast  
 RT cancer.";  
 RL Oncogene 17:3513-3519 (1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20225451; PubMed=10760572;  
 RA White G.R.M., Varley J.M., Heighway J.;  
 RT "Genomic structure and expression profile of LPHH1, a 7TM gene  
 RT variably expressed in breast cancer cell lines.";  
 RL Biochim. Biophys. Acta 1491:75-92(2000).  
 DR EMBL; AJ244509; CAB60204.1; -.  
 FT NON TER 1 1  
 FT NON TER 8 8  
 SQ SEQUENCE 8 AA; 1025 MW; 4D59D763344AAB08 CRC64;

Query Match 33.3%; Score 17; DB 4; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 NAYYL 9  
 | | | | |  
 DB 4 NKPFI 8

RESULT 3  
 Q96T78 PRELIMINARY; PRT; 9 AA.  
 AC Q96T78;  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Contactin-associated protein 2 (Fragment).  
 GN CNTNAP2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxId=9606;  
 RX MEDLINE=21250995; PubMed=11352571;  
 RA Nakabayashi K., Scherer S.W.;  
 RT "The human contactin-associated protein 2 (CNTNAP2) spans over 2 Mb of  
 RT DNA at chromosome 7q35.";  
 RL Genomics 73:108-112(2001).  
 DR EMBL; AF318295; AAK49906.1; -.  
 FT NON TER 1 1  
 FT NON TER 9 9  
 SQ SEQUENCE 9 AA; 1080 MW; 9139A2D5A77B51EA CRC64;

Query Match 33.3%; Score 17; DB 4; Length 9;  
 Best Local Similarity 33.3%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 FPNAPY 8  
 : | | | |  
 DB 4 YPSVSV 9

RESULT 4

P82429  
 ID P82429 PRELIMINARY; PRT; 9 AA.  
 AC P82429;  
 DT 01-JUN-2000 (TReMBLrel. 14, Created)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
 DE 44 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.  
 OC NCBI\_TaxId=4097;  
 RX MEDLINE=97061202; PubMed=9905232;  
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
 RA Samped G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
 RA Yano M., Horiuchi T.;  
 RT "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding  
 RT to the 12.7-28.0 min Region on the Linkage Map.";  
 RL DNA Res. 3:137-155(1996).  
 DR EMBL; D90705; BAA35310.1; -.  
 FT NON TER 1 1  
 FT NON TER 9 9  
 SQ SEQUENCE 8 AA; 964 MW; DF13B1DD04B476A CRC64;

Query Match 33.3%; Score 17; DB 10; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNAYL 9  
 | | | | |  
 DB 4 PQADPL 9

RESULT 5  
 Q9R7T2 PRELIMINARY; PRT; 8 AA.  
 AC Q9R7T2;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Hypothetical 1.0 kDa protein (Fragment).  
 GN YOG.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OC NCBI\_TaxId=562;  
 RX MEDLINE=97061202; PubMed=9905232;  
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
 RA Samped G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
 RA Yano M., Horiuchi T.;  
 RT "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding  
 RT to the 12.7-28.0 min Region on the Linkage Map.";  
 RL DNA Res. 3:137-155(1996).  
 DR EMBL; D90705; BAA35310.1; -.  
 FT NON TER 1 1  
 FT NON TER 8 8  
 SQ SEQUENCE 8 AA; 964 MW; DF13B1DD04B476A CRC64;

Query Match 31.4%; Score 16; DB 2; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 PYL 9  
 | | | | |  
 DB 2 PYI 4



RESULT 6

Q9P8E5 PRELIMINARY; PRT; 9 AA.

AC Q9P8E5;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE HIS4 protein (Fragment).

GN HIS4.

OS Kluyveromyces fragilis (Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

OX NCBI\_TaxID=28985;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NRRL-Y1140;

RX MEDLINE=99448382; PubMed=10518937;

RA Lamas-Macinas M., Esperanza Cerdan B., Freire-Picos M.A.;

RT "Kluyveromyces fragilis HIS4 transcriptional regulation: similarities

RT and differences to Saccharomyces cerevisiae HIS4 gene.";

RL FEBS Lett. 458:72-76(1999).

DR EMBL; AJ238494; CAB87125.1; -.

FT NON\_TER

FT SEQUENCE 9 AA; 1015 MW; 5770D2D772D2D767 CRC64;

Query Match 31.4%; Score 16; DB 3; Length 9;

Best Local Similarity 50.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 MFNPAP 7

DB 1 MLPVP 6

RESULT 7

Q9TWH6 PRELIMINARY; PRT; 8 AA.

AC Q9TWH6;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE BIOACTIVE peptide P4=PUTATIVE ESOPHAGEAL NEUROREGULATOR.

OS Perineura vancaurica.

OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculatea;

OC Phylloporidae; Metazoa; Annelida; Polychaeta; Palpata; Aciculatea;

OX NCBI\_TaxID=6355;

RN [1]

RP SEQUENCE.

RM MEDLINE=95323338; PubMed=7599979;

RA Takahashi T., Furukawa Y., Muneoka Y., Matsushima O., Ikeda T.,

RA Fujita T., Minakata H., Nomoto K.;

RT "Isolation and characterization of four novel bioactive peptides from

RT a polychaete annelid, Perineura vancaurica.";

RL Comp. Biochem. Physiol. C, Pharmacol. Toxicol. Endocrinol. 110:297-

RL 304(1995).

SO SEQUENCE 8 AA; 989 MW; 954772CAA87B0B59 CRC64;

Query Match 29.4%; Score 15; DB 5; Length 8;

Best Local Similarity 50.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 NAPP 8

DB 5 DVP 8

RESULT 8

Q8GTG5 PRELIMINARY; PRT; 8 AA.

AC Q8GTG5;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE WRKY transcription factor Iid-1 splice variant 2 (Fragment).

OS Lycopersicon esculentum (Tomato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; lamids; Solanales; Solanaceae; Solanum.

OX NCBI\_TaxID=4081;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Money Maker; TISSUE=Leaf;

RA Cagna G., Boes A., Ulker B., Zhou A., Wanke D., Somesich I.E.;

RT "Comparison of WRKY group II transcription factors from plants.";

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY157059; AA071729.1; -.

FT NON\_TER

FT SEQUENCE 8 AA; 917 MW; 59177B4775B87330 CRC64;

Query Match 29.4%; Score 15; DB 10; Length 8;

Best Local Similarity 66.7%; Pred. No. 8.3e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 APY 8

DB 4 SPY 6

RESULT 9

Q9UCS8 PRELIMINARY; PRT; 9 AA.

AC Q9UCS8;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Apolipoprotein A-I (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE.

RM MEDLINE=92075698; PubMed=1742316;

RA Ehnholm C., Bozas S.E., Tenkanen H., Kirszbaum L., Metso J.,

RA Murphy B., Walker I.D.;

RT "The apolipoprotein A-I binding protein of placenta and the SP-40,40

RT protein of human blood are different proteins which both bind to

RT apolipoprotein A-I.";

RL Biochim. Biophys. Acta 1086:255-260(1991).

FT NON\_TER

FT SEQUENCE 9 AA; 981 MW; 7FE37775A6C7776B CRC64;

Query Match 29.4%; Score 15; DB 4; Length 9;

Best Local Similarity 50.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PNPAP 7

DB 4 POSP 7

RESULT 10

Q9H522 PRELIMINARY; PRT; 9 AA.

AC Q9H522;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE BA90M5.3 (HCG-1) (Fragment).

GN BA90M5.3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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OX  NCBI_TaxID=9606;
RN  [1]
RA  SEQUENCE FROM N.A.
RL  Tromans A.;
DR  EMBL; AL139188; CAC15103.1; -.
FT  NON TER
SQ  SEQUENCE 9 AA; 951 MW; 96A3ADC72C455A5 CRC64;

Query Match
Best Local Similarity 29.4%; Score 15; DB 4; Length 9;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2 MFPNP 7
DB  1 MSSNP 6

RESULT 11
ID  Q9S8J8 PRELIMINARY; PRT; 9 AA.
AC  Q9S8J8;
DT  01-MAY-2000 (TREMBLrel. 13, Created)
DT  01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT  01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE  ORYZATENSIN-BIOACTIVE peptide.
OS  Oryza sativa (Rice).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC  Ehrhartoideae; Oryzeae; Oryza.
OX  NCBI_TaxID=4530;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=95102521; PubMed=7804141;
RA  Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;
RT  "Isolation and characterization of oryzatensin: a novel bioactive
RT  peptide with ileum-contracting and immunomodulating activities derived
RT  from rice albumin.";
RL  Biochem. Mol. Biol. Int. 33:1151-1158(1994).
DR  Grahame; Q9S8J8; -.
SQ  SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;

Query Match
Best Local Similarity 29.4%; Score 15; DB 10; Length 9;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  2 MFP 4
DB  4 MYP 6

RESULT 12
ID  Q98866 PRELIMINARY; PRT; 7 AA.
AC  Q98866;
DT  01-MAY-1999 (TREMBLrel. 10, Created)
DT  01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT  01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE  Cytochrome b/f subunit IV (Fragment).
OS  Spinacia oleracea (Spinach).
OC  Chloroplast.
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC  Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX  NCBI_TaxID=3562;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=86120353; PubMed=3003688;
RA  Sibben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.;
RT  "Spinach plastid genes coding for initiation factor IF-1, ribosomal
RT  protein S11 and RNA polymerase alpha-subunit.";
RL  Nucleic Acids Res. 14:1029-1044(1986).
DR  EMBL; X03496; CAA27215.1; -.

```

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KW  Chloroplast. 1
FT  NON TER
SQ  SEQUENCE 7 AA; 907 MW; 644729D77409C420 CRC64;

Query Match
Best Local Similarity 27.5%; Score 14; DB 8; Length 7;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  7 PYL 9
DB  4 PFL 6

RESULT 13
ID  Q07624 PRELIMINARY; PRT; 7 AA.
AC  Q07624;
DT  01-NOV-1996 (TREMBLrel. 01, Created)
DT  01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT  01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE  UORF1.
OS  Rous sarcoma virus (strain Prague C).
OC  Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX  NCBI_TaxID=11888;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=93010967; PubMed=1327749;
RA  Donze O., Spahr P.F.;
RT  "Role of the open reading frames of Rous sarcoma virus leader RNA in
RT  translation and genome packaging.";
RL  EMBO J. 11:3747-3757(1992).
DR  EMBL; X67587; CAA47862.1; -.
SQ  SEQUENCE 7 AA; 672 MW; 776045A7687DD6F0 CRC64;

Query Match
Best Local Similarity 27.5%; Score 14; DB 15; Length 7;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  4 PNPAP 7
DB  4 PSIP 7

RESULT 14
ID  P82858 PRELIMINARY; PRT; 8 AA.
AC  P82858;
DT  01-MAR-2001 (TREMBLrel. 16, Created)
DT  01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT  01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE  Uricase (EC 1.7.3.3) (urate oxidase) (Fragment).
OS  Puccinia recondita f. sp. triseti.
OC  Eukaryota; Fungi; Basidiomycota; Urediniomycetes; Urediniomycetidae;
OC  Uredinales; Pucciniaceae; Puccinia.
OX  NCBI_TaxID=142679;
RN  [1]
RP  SEQUENCE, FUNCTION, AND DEVELOPMENTAL STAGE.
RA  TISSUE=SPORE;
RA  Aguilar M., Montalbini P., Pineda M.;
RT  Submitted (NOV-2000) to the SWISS-PROT data bank.
CC  - FUNCTION: INVOLVED IN HOST-PARASITE RELATIONSHIP BETWEEN PLANTS
CC  AND FUNGI.
CC  - CATALYTIC ACTIVITY: URATE + O(2) + H(2)O = 5-HYDROXYISOURATE +
CC  H(2)O(2) (5-HYDROXYISOURATE DECOMPOSE TO FORM ALANTOIN).
CC  - SUBCELLULAR LOCATION: PEROXISOMAL (BY SIMILARITY).
CC  - DEVELOPMENTAL STAGE: GERMINATION.
CC  - SIMILARITY: BELONGS TO THE URICASE FAMILY.
CC  Interpro: IPR002042; Uricase.
DR  PROSITE; PS00366; URICASE; PARTIAL.
KW  Oxidoreductase; Purine metabolism; Peroxisome.
FT  NON TER
SQ  SEQUENCE 8 AA; 777 MW; 98C1ADD735B9D76D CRC64;

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Query Match 27.5%; Score 14; DB 3; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0;

QY 6 APY 8  
 ||:  
 1 APF 3

## RESULT 15

Q8W8G2 PRELIMINARY; PRT; 8 AA.  
 AC Q8W8G2:  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 GN COII.  
 OS Diadema savignyi (Longspine black urchin).  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinzoa;  
 OC Echinoidea; Euechinoidea; Diadematacea; Diadematoidea; Diadematiidae;  
 OC Diadema.  
 OX NCBI\_TaxID=105360;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DP751, SA2, SA7, SA10, GSA1, GSA3, GSA4, DOK17, and DOK105;  
 RX MEDLINE=21323357; PubMed=11430656;  
 RA Leesios H.A., Kessing B.D., Pearce J.S.;  
 RT "Population structure and speciation in tropical seas: global  
 phylogeography of the sea urchin Diadema";  
 RT Evolution 55:955-975 (2001).  
 RL Evolution 55:955-975 (2001).  
 DR EMBL; AY013065; AAL33860.1; -  
 DR EMBL; AY013080; AAL33861.1; -  
 DR EMBL; AY013083; AAL33862.1; -  
 DR EMBL; AY013086; AAL33863.1; -  
 DR EMBL; AY013088; AAL33864.1; -  
 DR EMBL; AY013090; AAL33865.1; -  
 DR EMBL; AY013091; AAL33867.1; -  
 DR EMBL; AY013102; AAL33868.1; -  
 DR EMBL; AY013103; AAL33869.1; -  
 KW Mitochondrion.  
 FT NON TER 1  
 SO SEQUENCE 8 AA; 1037 MM; 701B173B46DDC2D3 CRC64;

Query Match 27.5%; Score 14; DB 8; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0;

QY 6 APYL 9  
 ||:  
 3 AOYL 6

Search completed: January 21, 2004, 08:52:17  
 Job time : 36 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 21, 2004, 08:45:10 ; Search time 41 Seconds

(without alignments)  
34.842 Million cell updates/sec

Title: US-09-625-963A-1

Perfect score: 51

Sequence: 1 RMPNPAPYL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 179625

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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A\_Geneseq\_19Jun03:\*

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2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*

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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	9	21	AAV94202
2	51	100.0	9	21	AAV98670
3	51	100.0	9	21	AAV98778
4	51	100.0	9	21	AAV80200
5	51	100.0	9	22	AAU68769
6	51	100.0	9	22	AAU68877
7	51	100.0	9	22	AAV62002
8	51	100.0	9	22	AAV62110
9	51	100.0	9	23	ABG79100

10	51	100.0	9	23	ABG33239	Human WT1 immunoge
11	51	100.0	9	23	ABG33347	Mouse WT1 immunoge
12	51	100.0	9	23	AAE17298	Human Leukocyte an
13	47	92.2	9	21	AAV98523	WT1 derived immuno
14	47	92.2	9	22	AAU68622	Human Wilm's tumou
15	47	92.2	9	22	AAV61855	Human WT1 immunoge
16	47	92.2	9	23	ABG33092	Human WT1 immunoge
17	46	90.2	9	21	AAV98809	WT1 related peptid
18	46	90.2	9	22	AAU68908	Wilm's tumour prot
19	46	90.2	9	22	AAU62141	Human/mouse WT1 im
20	46	90.2	9	23	ABG33378	Human/mouse WT1 im
21	41	80.4	9	21	AAV98564	WT1 derived immuno
22	41	80.4	9	21	AAV98752	WT1 derived immuno
23	41	80.4	9	22	AAU68653	Human Wilm's tumou
24	41	80.4	9	22	AAU68851	Mouse Wilm's tumou
25	41	80.4	9	22	AAV61896	Human WT1 immunoge
26	41	80.4	9	22	AAV62084	Mouse WT1 immunoge
27	41	80.4	9	23	ABG33133	Human WT1 immunoge
28	41	80.4	9	23	ABG33321	Mouse WT1 immunoge
29	40	78.4	9	21	AAV98808	WT1 related peptid
30	40	78.4	9	22	AAU68907	Wilm's tumour prot
31	40	78.4	9	22	AAV62140	Human/mouse WT1 im
32	35	68.6	9	21	AAV98810	WT1 related peptid
33	35	68.6	9	22	AAU68909	Wilm's tumour prot
34	35	68.6	9	22	AAV62142	Human/mouse WT1 im
35	35	68.6	9	23	ABG33379	Human/mouse WT1 im
36	33	64.7	9	21	AAV98583	WT1 derived immuno
37	33	64.7	9	21	AAV98754	WT1 derived immuno
38	33	64.7	9	22	AAU68682	Human Wilm's tumou
39	33	64.7	9	22	AAU68853	Mouse Wilm's tumou
40	33	64.7	9	22	AAV61915	Human WT1 immunoge
41	33	64.7	9	22	AAV62086	Mouse WT1 immunoge
42	33	64.7	9	23	ABG33152	Human WT1 immunoge
43	33	64.7	9	23	ABG33323	Mouse WT1 immunoge
44	29	56.9	9	21	AAV98697	WT1 derived immuno
45	29	56.9	9	22	AAU68796	Human Wilm's tumou

#### ALIGNMENTS

RESULT 1	AAV94202	standard; peptide; 9 AA.
ID	AAV94202	
XX	AAV94202;	
AC	28-JUL-2000	(first entry)
XX		
DT	Human cytotoxic T lymphocyte-recognised WT1 peptide WT126-34.	
DE	WT126-3; peptide; epitope; Wilm's tumour gene; leukaemia;	
XX	breast cancer; melanoma; ovarian cancer; immunotherapy.	
KW	Homo sapiens.	
XX		
OS	WO200026249-A1.	
XX		
FN	11-MAY-2000.	
XX		
PD	02-NOV-1999;	99WO-GB03572.
XX		
PF	02-NOV-1998;	98GB-0023897.
XX		
PR	(IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.	
PA	Staubs HJ, Gao L;	
XX	WPI; 2000-376123/32.	
PI	Novel peptides comprising WT-1 and GATA-1 epitopes, their fragments or	
XX	variants, useful as vaccines for cancer immunotherapy	
DR		
XX		
PT		
XX		

PS Claim 1; Page 74; 93pp; English.  
XX  
XX The present sequence is peptide epitope WT126-34, produced by WT1  
CC expressing cells and found at residues 126-134 of the WT1 protein, which  
CC is recognized by cytotoxic T lymphocytes. WT1 is aberrantly expressed in  
CC leukemia, breast cancer, melanoma and ovarian cancer. The peptide can  
CC be used as a vaccine to stimulate the elimination, by cytotoxic T  
CC lymphocytes, of cancer cells aberrantly expressing WT1. In addition, the  
CC nucleic acid encoding the peptide may also be used in the same manner.  
CC Alternatively, the peptide may be used in vitro to produce activated  
CC cytotoxic T lymphocytes.  
XX  
SQ Sequence 9 AA;  
Query Match 100.0%; Score 51; DB 21; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 RMFPNAPYL 9  
DB 1 RMFPNAPYL 9  
RESULT 2  
AA98670  
ID AAY98670 standard; Peptide; 9 AA.  
XX  
XX AAY98670;  
AC  
XX  
XX 31-JUL-2000 (first entry)  
DT  
XX  
XX WT1 derived immunogenic peptide SEQ ID NO:185.  
DB  
XX  
XX WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;  
KW metastatic disease; mouse; human; Wilm's tumour; immune response;  
KM vaccine.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200018795-A2.  
PN  
XX  
XX 06-APR-2000.  
PD  
XX  
XX 30-SEP-1999; 99WO-US22819.  
PF  
XX  
XX 30-SEP-1998; 98US-0164223.  
PR  
XX 25-MAR-1999; 99US-0276484.  
PA  
XX (CORI-) CORIXA CORP.  
PI (GAIG/) GAIGER A.  
XX  
XX Gaiger A, Cheever M;  
PI  
XX  
XX WPI; 2000-293107/25.  
DR  
XX  
XX Novel polypeptides comprising an immunogenic portion of a native WT1  
PT polypeptide, useful for inhibiting the development of malignant  
PT diseases associated with WT1 expression e.g. leukemia or cancer -  
XX  
XX Claim 4; Page 171; 193pp; English.  
XX  
XX The present invention describes polypeptides (I) comprising an  
CC immunogenic portion of a native Wilm's Tumour gene product polypeptide,  
CC WT1, (or variants of the immunogenic portion retaining the ability to  
CC react with WT1-specific antisera and/or T-cell lines or clones) and  
CC comprising 16 consecutive amino acids (aa) or less of a native WT1  
CC polypeptide. The polypeptides are useful therapeutically and to  
CC manufacture medicaments for enhancing/inducing an immune response in  
CC patients. The polypeptides, mimetics or polynucleotides can be included  
CC with a carrier/excipient in pharmaceutical compositions or with a  
CC non-specific immune response enhancer (e.g. an adjuvant or enhancer  
CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical  
CC compositions and vaccines can be administered to human patients to

CC enhance or induce an immune response specific for WT1 or a cell  
CC expressing WT1, useful to inhibit the development of malignant diseases  
CC associated with WT1 expression, e.g. leukemia (especially acute/chronic  
CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially  
CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma).  
CC AAY98501 to AAY98811 represent polypeptide sequences, and AAY13848 to  
CC AAY13862 represent PCR primers, used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 9 AA;  
Query Match 100.0%; Score 51; DB 21; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 RMFPNAPYL 9  
DB 1 RMFPNAPYL 9  
RESULT 3  
AA98778  
ID AAY98778 standard; Peptide; 9 AA.  
XX  
XX AAY98778;  
AC  
XX  
XX 31-JUL-2000 (first entry)  
DT  
XX  
XX WT1 derived immunogenic peptide SEQ ID NO:293.  
DB  
XX  
XX WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;  
KW metastatic disease; mouse; human; Wilm's tumour; immune response;  
KM vaccine.  
XX  
XX Mus musculus.  
OS  
XX  
XX WO200018795-A2.  
PN  
XX  
XX 06-APR-2000.  
PD  
XX  
XX 30-SEP-1999; 99WO-US22819.  
PF  
XX  
XX 30-SEP-1998; 98US-0164223.  
PR  
XX 25-MAR-1999; 99US-0276484.  
PA  
XX (CORI-) CORIXA CORP.  
PI (GAIG/) GAIGER A.  
XX  
XX Gaiger A, Cheever M;  
PI  
XX  
XX WPI; 2000-293107/25.  
DR  
XX  
XX Novel polypeptides comprising an immunogenic portion of a native WT1  
PT polypeptide, useful for inhibiting the development of malignant  
PT diseases associated with WT1 expression e.g. leukemia or cancer -  
XX  
XX Claim 4; Page 186; 193pp; English.  
XX  
XX The present invention describes polypeptides (I) comprising an  
CC immunogenic portion of a native Wilm's Tumour gene product polypeptide,  
CC WT1, (or variants of the immunogenic portion retaining the ability to  
CC react with WT1-specific antisera and/or T-cell lines or clones) and  
CC comprising 16 consecutive amino acids (aa) or less of a native WT1  
CC polypeptide. The polypeptides are useful therapeutically and to  
CC manufacture medicaments for enhancing/inducing an immune response in  
CC patients. The polypeptides, mimetics or polynucleotides can be included  
CC with a carrier/excipient in pharmaceutical compositions or with a  
CC non-specific immune response enhancer (e.g. an adjuvant or enhancer  
CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical  
CC compositions and vaccines can be administered to human patients to  
CC enhance or induce an immune response specific for WT1 or a cell  
CC expressing WT1, useful to inhibit the development of malignant diseases  
CC associated with WT1 expression, e.g. leukemia (especially acute/chronic

CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially  
 CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma).  
 CC AA98801 to AA98811 represent polypeptide sequences, and AA13848 to  
 CC AA13862 represent PCR primers, used in the exemplification of the  
 CC present invention.

CC Sequence 9 AA;

Query Match 100.0%; Score 51; DB 21; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMFPNAPYL 9  
 |||||  
 Db 1 RMFPNAPYL 9

#### RESULT 4

ID AA980200 standard; Peptide; 9 AA.

AC AA980200;

DT 24-MAY-2000 (first entry)

DE Human Wilm's tumour suppressor gene WT1 product peptide SEQ ID NO:5.

KW Wilm's tumour suppressor gene; WT1; cancer; antigen; vaccine; MHC;  
 KW major histocompatibility complex; leukaemia; tumour; antitumour.

XX Homo sapiens.

OS WO200006602-A1.

PN 10-FEB-2000.

PF 30-JUL-1999; 99WO-JP04130.

PR 31-JUL-1998; 98JP-0218093.

PA (SUGI/) SUGIYAMA H.

PI Sugiyama H, Oka Y;

DR WPI; 2000-195264/17.

CC Cancer antigens based on Wilm's tumor suppressor gene WT1 product or  
 PT peptide derivatives, for cancer vaccines in treating leukemia and solid  
 PT tumors e.g. stomach cancer, skin cancer, lung cancer and breast cancer  
 XX Claim 5; Page 18; 48pp; Japanese.

CC The present invention describes a cancer antigen containing the active  
 CC component of Wilm's tumour suppressor gene WT1 product, or partial  
 CC peptides, for cancer vaccines in treating leukemia and solid tumours.  
 CC The cancer antigens are useful for cancer vaccines in treating  
 CC leukaemia, bone-marrow abnormal formation syndrome, malignant lymphoma,  
 CC multiple myeloma, stomach cancer, cancer of the large intestine, lung  
 CC cancer, breast cancer, blastoma, liver cancer, skin cancer, bladder  
 CC cancer, prostate cancer, uterus cancer, cervical cancer, or ovary  
 CC cancer. The present sequence represents a peptide from the human  
 CC Wilm's tumour suppressor gene WT1 product.

CC Sequence 9 AA;

Query Match 100.0%; Score 51; DB 21; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMFPNAPYL 9  
 |||||  
 Db 1 RMFPNAPYL 9

#### RESULT 5

ID AAU68769 standard; Peptide; 9 AA.

AC AAU68769;

DT 16-JAN-2002 (first entry)

DE Human Wilm's tumour protein, WT1, antigenic peptide #164.

KW Human; Wilm's tumour; WT1; pleural mesothelioma; antigen;  
 KW leukaemia; acute myeloid leukaemia; ALL; chronic myeloid leukaemia; CML;  
 KW acute lymphocytic leukaemia; ALL; myelodysplastic syndromes;  
 KW myeloproliferative syndrome; cancer; cytostatic.

OS Homo sapiens.

PN WO200162920-A2.

PD 30-AUG-2001.

PF 22-FEB-2001; 2001WO-US05702.

PR 22-FEB-2000; 2000US-184070P.

PA (CORI-) CORIXA CORP.

PI Cheever MA, Galger A;

DR WPI; 2001-648218/74.

CC Composition for the treatment of mesothelioma comprises specific  
 PT peptides i.e. Wilm's tumour antigen polypeptide derived antigenic  
 PT fragments -

XX Claim 1; Page 176; 242pp; English.

CC The invention relates to the use of a composition comprising at least a  
 CC first isolated peptide, of between 9 and 40 amino acids or a first  
 CC nucleic acid, encoding the peptide, in the manufacture of a medicament  
 CC for treating or preventing mesothelioma. The peptides are antigenic  
 CC peptides derived from the Wilm's tumour protein WT1. The composition is  
 CC useful for the treatment of mesothelioma, Wilm's tumour, preferably  
 CC pleural mesothelioma and other WT1 associated malignancies e.g.  
 CC leukaemia (including acute myeloid leukaemia, ALL, chronic myeloid  
 CC leukaemia, CML, acute lymphocytic leukaemia, ALL, and childhood ALL),  
 CC myelodysplastic syndromes, myeloproliferative syndromes and cancers  
 CC (e.g. breast, testicular, prostate, lung and ovarian) in mammals,  
 CC preferably humans. The present sequence is an antigenic peptide of  
 CC the invention derived from human WT1.

CC Sequence 9 AA;

Query Match 100.0%; Score 51; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RMFPNAPYL 9  
 |||||  
 Db 1 RMFPNAPYL 9

#### RESULT 6

ID AAU68877 standard; Peptide; 9 AA.

AC AAU68877;

DT 16-JAN-2002 (first entry)

DE Mouse Wilm's tumour protein, WT1, antigenic peptide #46.

XX	Mouse; Wilms' tumour; WT1; pleural mesothelioma; antigen;	
KW	Leukemia; acute myeloid leukaemia; ALL; chronic myeloid leukaemia; CML;	
KM	acute lymphocytic leukaemia; ALL; myelodysplastic syndromes;	
KX	myeloproliferative syndrome; cancer; cytostatic.	
XX		
OS	Mus musculus.	
XX		
PN	WO200162920-A2.	
XX		
PD	30-AUG-2001.	
XX		
XX		
PF	22-FEB-2001; 2001WO-US05702.	
XX		
XX		
PR	22-FEB-2000; 2000US-184070P.	
XX		
XX		
PA	(CORI-) CORIXA CORP.	
XX		
PI	Cheever MA, Gaiger A;	
XX		
DR	WPI; 2001-648218/74.	
XX		
PT	Composition for the treatment of mesothelioma comprises specific	
PT	peptides i.e. Wilms' tumour antigen polypeptide derived antigenic	
PT	fragments -	
XX		
PS	Claim 1; Page 24; 242pp; English.	
XX		
CC	The invention relates to the use of a composition comprising at least a	
CC	first isolated peptide, of between 9 and 40 amino acids or a first	
CC	nucleic acid, encoding the peptide, in the manufacture of a medicament	
CC	for treating or preventing mesothelioma. The peptides are antigenic	
CC	peptides derived from the Wilms' tumour protein WT1. The composition is	
CC	useful for the treatment of mesothelioma, Wilms' tumour, preferably	
CC	pleural mesothelioma and other WT1 associated malignancies e.g.	
CC	leukaemia (including acute myeloid leukaemia, ALL, chronic myeloid	
CC	leukaemia, CML, acute lymphocytic leukaemia, ALL, and childhood ALL),	
CC	myelodysplastic syndromes, myeloproliferative syndromes and cancers	
CC	(e.g. breast, testicular, prostate, lung and ovarian) in mammals,	
CC	preferably humans. The present sequence is an antigenic peptide of	
CC	the invention derived from mouse WT1.	
XX		
XX		
SO	Sequence 9 AA;	
	Query Match 100.0%; Score 51; DB 22; Length 9;	
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;	
	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 RMFPNAPYL 9	
Db	1 RMFPNAPYL 9	
RESULT 7		
AAAG62002		
ID	AAAG62002 standard; Peptide; 9 AA.	
XX		
AC	AAAG62002;	
XX		
DT	06-JUL-2001 (first entry)	
XX		
DE	Human WT1 immunogenic peptide SEQ ID NO: 185.	
XX		
KW	Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;	
KM	chromosome 11p13; zinc finger transcription factor.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200125273-A2.	
XX		
PD	12-APR-2001.	
XX		
PF	04-OCT-2000; 2000WO-US27465.	
XX		

```
PR    04-OCT-1999;      99US-0157459.
XX
XX   (CORI-) CORIXA CORP.
PA
XX   Skeiky YAM, Xu J, Cheever MA, Reed SG;
XX   WPI; 2001-328324/34.
DR
XX   Polypeptide comprising part of the Wilms's Tumour gene product sequence is
XX   used in the diagnosis and treatment of malignant diseases e.g. leukemia
PT   and cancer associated with WT1 -
PS
XX   Claim 4; Page 183; 228pp; English.
CC
XX   The present invention describes compositions comprising peptides derived
CC   from the Wilm's tumour protein WT1 and methods for their use in treating
CC   malignant diseases. Peptides derived from both the murine and human WT1
CC   proteins are provided. The human WT1 gene is found on chromosome 11p13.
CC   and the protein was shown to be a zinc finger transcription factor. The
CC   immunogenic peptides of the invention are particularly useful in the
CC   diagnosis and treatment of cancer and leukaemia. The present sequence is
CC   a polypeptide described in the exemplification of the invention.
SQ
Sequence       9 AA;

QY        Query Match                100.0%; Score 51; DB 22; Length 9;
          Best Local Similarity     100.0%; Pred. No. 9.3e+05;
          Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
DB         1 RMPFNAPYL 9
           |||||
           1 RMPFNAPYL 9

RESULT 8
AAG62110
ID AAG62110 standard; Peptide; 9 AA.
AC AAG62110;
XX
XX   06-JUL-2001 (first entry)
DT
XX
XX   Mouse WT1 immunogenic peptide SEQ ID NO: 293.
DE
XX
XX   Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilms's tumour gene;
KM   chromosome 11p13; zinc finger transcription factor.
KW
XX
XX   Mus musculus.
OS
XX   WO200125273-A2.
PN
XX   12-APR-2001.
PD
XX
XX   04-OCT-2000; 2000WO-US27465.
PF
XX   04-OCT-1999; 99US-0157459.
PR
XX   (CORI-) CORIXA CORP.
PA
XX
XX   Skeiky YAM, Xu J, Cheever MA, Reed SG;
PI
XX   WPI; 2001-328324/34.
DR
XX
XX   Polypeptide comprising part of the Wilms's Tumour gene product sequence is
PT   used in the diagnosis and treatment of malignant diseases e.g. leukemia
PT   and cancer associated with WT1 -
PS
XX
XX   Claim 4; Page 200; 228pp; English.
```



CC and the protein was shown to be a zinc finger transcription factor. The  
CC immunogenic peptides of the invention are particularly useful in the  
CC diagnosis and treatment of cancer and leukaemia. The present sequence is  
CC a polypeptide described in the exemplification of the invention.

XX Sequence 9 AA;

XX Query Match 100.0%; Score 51; DB 23; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 RMFPNAPYL 9

RESULT 9

ABG79100 ABG79100 standard; Peptide; 9 AA.

AC ABG79100;

DT 15-NOV-2002 (first entry)

XX Human WT1 class I HLA widely expressed antigen peptide #1.

XX Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;  
XX lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;  
XX Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;  
XX kidney cancer; adenocarcinoma; breast cancer; prostate cancer;  
XX ovarian cancer; pancreatic cancer; epiglottis; vaccine; dendritic cell;  
XX tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;  
XX cytostatic; human.

XX Homo sapiens.

XX WO200264057-A2.

XX 22-AUG-2002.

XX 15-FEB-2002; 2002WO-US05212.

XX 15-FEB-2001; 2001US-268687P.

XX (BAYU ) BAYLOR COLLEGE MEDICINE.

XX Wang R;

XX WPI; 2002-627577/67.

XX Novel composition for treating a disease in an animal, comprises an  
XX immune effector cell and cell penetrating peptide associated with an  
XX antigen or antibody -

XX Disclosure; Page 19; 61pp; English.

XX The invention relates to a composition (I) comprising an immune effector  
XX cell and a cell penetrating peptide (CPP) associated with an antigen or  
XX antibody. Also included are (1) a vaccine comprising (I), CPP  
XX associated with an antigen, and a pharmaceutically acceptable carrier  
XX and (2) preparing a composition for a disease, by providing (I)  
XX and CPP associated with an antigen for a disease, and introducing the  
XX antigen-associated CPP to (1), where antigen enters into the cell.  
XX The antigens are, for example, tumour antigen derived epitopes  
XX recognised by tumour infiltrating lymphocytes (TIL) of HLA (human  
XX leukocyte antigen) class I or II. The composition is useful for enhancing  
XX immunity in an animal to a disease, by administering a mature dendritic  
XX cell comprising CPP associated with an antigen to a disease, to the animal,  
XX such that following the administration, animal is protected from disease,  
XX where the animal comprises both CD4+ and CD8+ T cells. It is also useful  
XX for treating a disease (e.g., cancer, tumour, melanoma, lymphoma,  
XX lymphoma, sarcoma, lung cancer, non-Hodgkin's lymphoma, leukaemia,  
XX Hodgkin's lymphoma, uterine cancer, cervical cancer, bladder cancer,

CC kidney cancer, adenocarcinoma, breast cancer, prostate cancer,  
CC ovarian cancer and pancreatic cancer). The animal is further subjected to  
CC a cancer treatment including surgery, radiation, chemotherapy or gene  
CC therapy. The administration of (I), preferably dendritic cell is prior  
CC to, subsequent to or concurrent with, the cancer treatment. The present  
CC sequence is a tumour antigen derived epitope for inclusion in the  
CC composition of the invention.

XX Sequence 9 AA;

XX Query Match 100.0%; Score 51; DB 23; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 RMFPNAPYL 9

RESULT 10

ABG33239 ABG33239 standard; Peptide; 9 AA.

AC ABG33239;

DT 15-JUL-2002 (first entry)

XX Human WT1 immunogenic peptide #162.

XX Human; mouse; cytostatic; immunostimulant; WT1; cancer;  
XX immune response.

XX Homo sapiens.

XX WO200228414-A1.

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US31139.

XX 06-OCT-2000; 2000US-0684361.

XX 09-OCT-2000; 2000US-0685830.

XX 15-FEB-2001; 2001US-0785019.

XX 24-AUG-2001; 2001US-0938864.

XX (CORI-) CORIXA CORP.

XX (GAIG-) GAIGER A.

XX Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedrick TS;

XX Sleach PR, Mossman S, Evans L, Spies AG, Boydston J;

XX WPI; 2002-352217/38.

XX Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for  
XX treating and diagnosing cancer in a patient -  
XX Example 4; Page 194; 260pp; English.  
XX The invention relates to an isolated WT1 polynucleotide (I) and  
XX polypeptide encoded by (I). The WT1 polynucleotides and polypeptides  
XX are used for treating and detecting cancer in a patient, and for  
XX stimulating an immune response in patient. ABG33070-ABG33405  
XX represent WT1 amino acid sequences of the invention.

XX Sequence 9 AA;

XX Query Match 100.0%; Score 51; DB 23; Length 9;

XX Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 1 RMFPNAPYL 9

```

RESULT 11
ABG33347
ID ABG33347 standard; Peptide; 9 AA.
AC ABG33347;
XX
XX 15-JUL-2002 (first entry)
XX
DE Mouse WT1 immunogenic peptide #44.
XX
XX Human; mouse; cytostatic; immunostimulant; WT1; cancer;
XX immune response.
XX
XX Mus musculus.
XX
XX WO200228414-A1.
XX
XX 11-APR-2002.
XX
XX 03-OCT-2001; 2001WO-US31139.
XX
XX 06-OCT-2000; 2000US-0684361.
XX 09-OCT-2000; 2000US-0685830.
XX 15-FEB-2001; 2001US-0785019.
XX 24-AUG-2001; 2001US-0938864.
XX
XX (CORI-) CORIXA CORP.
XX (GAIG/) GAIGER A.
XX
XX Gaiger A, McNeill M, Moulton G, Vedvick TS;
XX Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX WPI; 2002-352217/38.
XX
XX Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
XX treating and diagnosing cancer in a patient -
XX
XX Example 4; Page 210; 260pp; English.
XX
XX The invention relates to an isolated WT1 polynucleotide (I) and
XX polypeptide encoded by (I). The WT1 polynucleotides and polypeptides
XX are used for treating and detecting cancer in a patient, and for
XX stimulating an immune response in patient. ABG33070-ABG33405
XX represent WT1 amino acid sequences of the invention.
XX
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 51; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RMFPNAPYL 9
DB 1 RMFPNAPYL 9

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RESULT 12
AAE17298
ID AAE17298 standard; peptide; 9 AA.
AC AAE17298;
XX
XX 18-APR-2002 (first entry)
XX
XX Human leukocyte antigen (HLA-A2.1) restricted peptide. Db126.
XX
XX Human; artificial antigen presenting cell; AAPC; beta2-microglobulin;
XX human leukocyte antigen; HLA; major histocompatibility complex; MHC;
XX cytotoxic T lymphocyte; CTL; T cell-specific antigen; TCA; antitumour;
XX immune response; cancer.
XX

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OS Homo sapiens.
XX
XX WO200194944-A2.
XX
XX 13-DEC-2001.
XX
XX 01-JUN-2001; 2001WO-US17981.
XX
XX 02-JUN-2000; 2000US-209157P.
XX
XX (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
XX Sadelain M, Latouche J;
XX
XX WPI; 2002-139667/18.
XX
XX Artificial antigen presenting cells for activating T lymphocytes,
XX comprising eukaryotic cell expressing antigen presenting complex having
XX beta2-microglobulin, exogenous accessory molecule, human leukocyte
XX antigen molecule and protein -
XX
XX Example 17; Page 40; 75pp; English.
XX
XX The present invention relates to an artificial antigen presenting cell
XX (AAPC) comprising a eukaryotic cell expressing an antigen presenting
XX complex comprising beta2-microglobulin, an exogenous accessory molecule,
XX a human leukocyte antigen, HLA (major histocompatibility complex, MHC)
XX molecule of a single type and a protein that is processed intracellularly
XX to produce an exogenous T cell-specific epitope. The invention also
XX relates to methods for activation of T lymphocytes. The method is also
XX useful for identifying within a test population of cytotoxic T
XX lymphocytes (CTLs), CTLs specifically activated against a known T-cell
XX specific antigen (TCA), which is useful for diagnostic purposes. AAPC is
XX also useful for activating CTLs, by contacting AAPC with a suitable
XX population of T lymphocytes under conditions suitable for the activation
XX and isolating the activated CTLs. AAPC is further useful for the
XX investigation of primary T cell activation and diagnostic applications
XX here primary T cell activation allow discovery of antigens and accessory
XX molecules, and diagnostic applications include cell-based assays for
XX quantifying immune response in normal, infected or treated (vaccinated)
XX patients. Composition comprising AAPC or activated T cells produced by
XX utilising AAPC is useful for eliciting an antitumour response. The
XX invention is used for the treatment of cancer. The present sequence is
XX human HLA-A2.1 restricted peptide used in additional AAPC-induced CTL-
XX activation.
XX
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 51; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RMFPNAPYL 9
DB 1 RMFPNAPYL 9

```

```

RESULT 13
AAV98523
ID AAV98523 standard; peptide; 9 AA.
AC AAV98523;
XX
XX 31-JUL-2000 (first entry)
XX
XX WT1 derived immunogenic peptide SEQ ID NO:38.
XX
XX WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;
XX metastatic disease; mouse; human; Wilms' tumour; immune response;
XX vaccine.
XX
XX Homo sapiens.
XX

```

PN WO200018795-A2.  
 XX  
 PD 06-APR-2000.  
 XX  
 PF 30-SEP-1999; 99WO-US22819.  
 XX  
 PR 30-SEP-1998; 98US-0164223.  
 XX  
 PR 25-MAR-1999; 99US-0276484.  
 XX  
 PA (CORI-) CORIYA CORP.  
 XX (GAIG/) GAIGER A.  
 PA  
 PI Gaiger A, Cheever M;  
 XX  
 DR WPI; 2000-293107/25.  
 XX  
 PT Novel polypeptides comprising an immunogenic portion of a native WTI  
 XX polypeptide, useful for inhibiting the development of malignant  
 PS diseases associated with WTI expression e.g. leukemia or cancer  
 XX  
 PS Claim 4; Page 149; 193pp; English.  
 XX  
 XX The present invention describes polypeptides (1) comprising an  
 CC immunogenic portion of a native Wilm's Tumour gene product polypeptide,  
 CC WTI, (or variants of the immunogenic portion retaining the ability to  
 CC react with WTI-specific antisera and/or T-cell lines or clones) and  
 CC comprising 16 consecutive amino acids (aa) or less of a native WTI  
 CC polypeptide. The polypeptides are useful therapeutically and to  
 CC manufacture medicaments for enhancing/inducing an immune response in  
 CC patients. The polypeptides, mimetics or polynucleotides can be included  
 CC with a carrier/excipient in pharmaceutical compositions or with a  
 CC non-specific immune response enhancer (e.g. an adjuvant or enhancer  
 CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical  
 CC compositions and vaccines can be administered to human patients to  
 CC enhance or induce an immune response specific for WTI or a cell  
 CC expressing WTI, useful to inhibit the development of malignant diseases  
 CC associated with WTI expression, e.g. leukemia (especially acute/chronic  
 CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially  
 CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma).  
 CC AA098501 to AA098811 represent polypeptide sequences, and AA013848 to  
 CC AA013862 represent PCR primers, used in the exemplification of the  
 CC present invention.  
 CC  
 XX Sequence 9 AA;  
 XX  
 XX Query Match 92.2%; Score 47; DB 21; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 XX  
 XX 1 RMFPNAPY 8  
 XX |||||  
 XX 2 RMFPNAPY 9  
 XX  
 XX RESULT 14  
 XX AA068622  
 XX ID AA068622 standard; Peptide; 9 AA.  
 XX  
 XX AC AA068622;  
 XX  
 XX DT 16-JAN-2002 (first entry)  
 XX  
 XX DE Human Wilm's tumour protein, WTI, antigenic peptide #17.  
 XX  
 XX KW Human, Wilm's tumour; WTI; pleural mesothelioma; antigen;  
 XX leukaemia; acute myeloid leukaemia; ALL; chronic myeloid leukaemia; CML;  
 XX acute lymphocytic leukaemia; ALL; myelodysplastic syndromes;  
 XX myeloproliferative syndrome; cancer; cytostatic.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX WO2000162920-A2.  
 XX

[illegible]

PT used in the diagnosis and treatment of malignant diseases e.g. leukemia  
PT and cancer associated with WTI -

XX  
PS Claim 4; Page 161; 228pp; English.

XX  
CC The present invention describes compositions comprising peptides derived  
CC from the Wilm's tumour protein WTI and methods for their use in treating  
CC malignant diseases. Peptides derived from both the murine and human WTI  
CC proteins are provided. The human WTI gene is found on chromosome 11p13,  
CC and the protein was shown to be a zinc finger transcription factor. The  
CC immunogenic peptides of the invention are particularly useful in the  
CC diagnosis and treatment of cancer and leukemia. The present sequence is  
CC a polypeptide described in the exemplification of the invention.

XX  
SQ Sequence 9 AA;

Query Match 92.2%; Score 47; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPY 8  
Db 2 RMFPNAPY 9

Search completed: January 21, 2004, 08:51:04  
Job time : 41 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 21, 2004, 08:52:21 : Search time 32 Seconds  
(without alignments)  
57.510 Million cell updates/sec

Title: US-09-625-963A-1  
Perfect score: 51  
Sequence: 1 RMPFNAPYL 9

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 762491 seqs, 204481190 residues  
Total number of hits satisfying chosen parameters: 81252

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEM\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEM\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEM\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEM\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEM\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEM\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	9	US-09-872-832-46	Sequence 46, App1
2	51	100.0	9	US-09-938-864-185	Sequence 185, App
3	51	100.0	9	US-09-938-864-293	Sequence 293, App
4	51	100.0	9	US-09-791-477-185	Sequence 185, App
5	51	100.0	9	US-09-791-477-293	Sequence 293, App
6	51	100.0	9	US-09-785-019-185	Sequence 185, App
7	51	100.0	9	US-09-785-019-293	Sequence 293, App
8	51	100.0	9	US-10-210-148-54	Sequence 54, App1
9	51	100.0	9	US-10-195-835-185	Sequence 185, App
10	51	100.0	9	US-10-195-835-293	Sequence 293, App
11	51	100.0	9	US-10-286-333-185	Sequence 185, App
12	51	100.0	9	US-10-286-333-293	Sequence 293, App
13	51	100.0	9	US-10-244-830-185	Sequence 185, App
14	51	100.0	9	US-10-244-830-293	Sequence 293, App
15	51	100.0	9	US-10-125-635A-185	Sequence 185, App

16	51	100.0	9	US-10-125-635A-293	Sequence 293, App
17	51	100.0	9	US-10-002-603-185	Sequence 185, App
18	51	100.0	9	US-10-002-603-293	Sequence 293, App
19	47	92.2	9	US-09-938-864-38	Sequence 38, App1
20	47	92.2	9	US-09-791-477-38	Sequence 38, App1
21	47	92.2	9	US-09-785-019-38	Sequence 38, App1
22	47	92.2	9	US-10-195-835-38	Sequence 38, App1
23	47	92.2	9	US-10-286-333-38	Sequence 38, App1
24	47	92.2	9	US-10-244-830-38	Sequence 38, App1
25	47	92.2	9	US-10-125-635A-38	Sequence 38, App1
26	47	92.2	9	US-10-002-603-38	Sequence 38, App1
27	46	90.2	9	US-09-938-864-324	Sequence 324, App
28	46	90.2	9	US-09-791-477-324	Sequence 324, App
29	46	90.2	9	US-09-785-019-324	Sequence 324, App
30	46	90.2	9	US-10-195-835-324	Sequence 324, App
31	46	90.2	9	US-10-286-333-324	Sequence 324, App
32	46	90.2	9	US-10-244-830-324	Sequence 324, App
33	46	90.2	9	US-10-125-635A-324	Sequence 324, App
34	46	90.2	9	US-10-002-603-324	Sequence 324, App
35	41	80.4	9	US-09-938-864-79	Sequence 79, App1
36	41	80.4	9	US-09-791-477-79	Sequence 79, App1
37	41	80.4	9	US-09-785-019-79	Sequence 79, App1
38	41	80.4	9	US-10-195-835-79	Sequence 79, App1
39	41	80.4	9	US-10-286-333-79	Sequence 79, App1
40	41	80.4	9	US-10-244-830-79	Sequence 79, App1
41	41	80.4	9	US-10-125-635A-79	Sequence 79, App1
42	41	80.4	9	US-10-002-603-79	Sequence 79, App1
43	41	80.4	9	US-10-286-333-267	Sequence 267, App
44	41	80.4	9	US-10-244-830-267	Sequence 267, App
45	41	80.4	9	US-10-125-635A-267	Sequence 267, App

#### ALIGNMENTS

RESULT 1  
US-09-872-832-46  
Sequence 46, Application US/09872832  
Patent No. US20020131960A1  
GENERAL INFORMATION:  
APPLICANT: Memorial Sloan-Kettering Cancer Center  
TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE THEREOF  
FILE REFERENCE: 830002-2003.1  
CURRENT APPLICATION NUMBER: US/09/872,832  
CURRENT FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: 60/209,157  
PRIOR FILING DATE: 2000-02-06  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 46  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-872-832-46

Query Match 100.0%; Score 51; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMPFNAPYL 9  
|||  
Db 1 RMPFNAPYL 9

RESULT 2  
US-09-938-864-185  
Sequence 185, Application US/09938864  
Publication No. US20030072767A1  
GENERAL INFORMATION:  
APPLICANT: Gauger, Alexander  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Smithgall, Molly  
APPLICANT: Moulton, Gus

```

; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 185
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-185

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```

Query Match      100.0%; Score 51; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RMFPNAPYL 9
Db 1 RMFPNAPYL 9

```

```

RESULT 3
US-09-938-864-293

```

```

; Sequence 293, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-938-864-293

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; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-938-864-293

```

```

Query Match      100.0%; Score 51; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RMFPNAPYL 9
Db 1 RMFPNAPYL 9

```

```

RESULT 4
US-09-791-477-185

```

```

; Sequence 185, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS

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; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 185
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-185

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Query Match      100.0%; Score 51; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RMFPNAPYL 9
Db 1 RMFPNAPYL 9

```

```

RESULT 5
US-09-791-477-293

```

```

; Sequence 293, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-477-293

```

```

Query Match      100.0%; Score 51; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RMFPNAPYL 9
Db 1 RMFPNAPYL 9

```

```

RESULT 6
US-09-785-019-185

```

```

; Sequence 185, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0

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SEQ ID NO 185  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-785-019-185

Query Match 100.0%; Score 51; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
|||||  
DB 1 RMFPNAPYL 9

RESULT 7  
US-09-785-019-293  
Sequence 293, Application US/09785019  
Publication No. US20030082196A1  
GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander  
APPLICANT: Cheever, Martin A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Smithgall, Molly  
APPLICANT: Moulton, Gus  
APPLICANT: Vedvick, Thomas S.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1

FILE REFERENCE: 210121.465C4

CURRENT FILING DATE: 2001-02-15

NUMBER OF SEQ ID NOS: 376

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 293

LENGTH: 9

TYPE: PRT

ORGANISM: Mus musculus

US-09-785-019-293

Query Match 100.0%; Score 51; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
|||||  
DB 1 RMFPNAPYL 9

RESULT 8  
US-10-210-148-54  
Sequence 54, Application US/10210148  
Publication No. US20030171280A1  
GENERAL INFORMATION:

APPLICANT: Sodestrom, Karl Peter  
TITLE OF INVENTION: Compositions And Methods For Modulation Of Immune Response

FILE REFERENCE: TROM0002

CURRENT FILING DATE: 2002-07-31

PRIOR APPLICATION NUMBER: PCT/US02/24311

PRIOR FILING DATE: 2002-07-31

NUMBER OF SEQ ID NOS: 117

SOFTWARE: Patencin version 3.2

SEQ ID NO 54

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

US-10-210-148-54

Query Match 100.0%; Score 51; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
|||||  
DB 1 RMFPNAPYL 9

RESULT 9  
US-10-195-835-185  
Sequence 185, Application US/10195835  
Publication No. US20030198622A1  
GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander  
APPLICANT: Smithgall, Molly D.  
APPLICANT: Carter, Patrick  
APPLICANT: Cheever, Martin A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Sutherland, R. Alec  
APPLICANT: Mossman, Sally P.  
APPLICANT: Evans, Lawrence S.  
APPLICANT: Swanson, Ryan M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1

FILE REFERENCE: 210121.465C8

CURRENT FILING DATE: 2002-07-12

NUMBER OF SEQ ID NOS: 461

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 185

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapien

US-10-195-835-185

Query Match 100.0%; Score 51; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9  
|||||  
DB 1 RMFPNAPYL 9

RESULT 10  
US-10-195-835-293  
Sequence 293, Application US/10195835  
Publication No. US20030198622A1  
GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander  
APPLICANT: Smithgall, Molly D.  
APPLICANT: Carter, Patrick  
APPLICANT: Cheever, Martin A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Sutherland, R. Alec  
APPLICANT: Mossman, Sally P.  
APPLICANT: Evans, Lawrence S.

APPLICANT: Swanson, Ryan M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1

FILE REFERENCE: 210121.465C8

CURRENT FILING DATE: 2002-07-12

NUMBER OF SEQ ID NOS: 461

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 293

LENGTH: 9

TYPE: PRT

ORGANISM: Mus musculus

US-10-195-835-293

Query Match 100.0%; Score 51; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RMFPNAPYL 9

Db 1 RMFPNAPYL 9

RESULT 11

US-10-286-333-185  
 ; Sequence 185, Application US/10286333  
 ; Publication No. US20030215458A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Java, No. US20030215458A1a1ie  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
 ; FILE REFERENCE: 210121.465C10  
 ; CURRENT APPLICATION NUMBER: US/10/286,333  
 ; CURRENT FILING DATE: 2002-10-30  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 185  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 US-10-286-333-185

Query Match 100.0%; Score 51; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9

Db 1 RMFPNAPYL 9

RESULT 12

US-10-286-333-293  
 ; Sequence 293, Application US/10286333  
 ; Publication No. US20030215458A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Java, No. US20030215458A1a1ie  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
 ; FILE REFERENCE: 210121.465C10  
 ; CURRENT APPLICATION NUMBER: US/10/286,333  
 ; CURRENT FILING DATE: 2002-10-30  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 293  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-286-333-293

Query Match 100.0%; Score 51; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9

Db 1 RMFPNAPYL 9

RESULT 13

US-10-244-830-185  
 ; Sequence 185, Application US/10244830  
 ; Publication No. US20030235557A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Cheever, Martin A.  
 ; APPLICANT: Java, No. US20030235557A1a1ie  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY

FILE REFERENCE: 210121.465C9  
 ; CURRENT APPLICATION NUMBER: US/10/244,830  
 ; CURRENT FILING DATE: 2002-09-16  
 ; NUMBER OF SEQ ID NOS: 468  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 185  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 US-10-244-830-185

Query Match 100.0%; Score 51; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9

Db 1 RMFPNAPYL 9

RESULT 14

US-10-244-830-293  
 ; Sequence 293, Application US/10244830  
 ; Publication No. US20030235557A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Cheever, Martin A.  
 ; APPLICANT: Java, No. US20030235557A1a1ie  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
 ; FILE REFERENCE: 210121.465C9  
 ; CURRENT APPLICATION NUMBER: US/10/244,830  
 ; CURRENT FILING DATE: 2002-09-16  
 ; NUMBER OF SEQ ID NOS: 468  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 293  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-244-830-293

Query Match 100.0%; Score 51; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMFPNAPYL 9

Db 1 RMFPNAPYL 9

RESULT 15

US-10-125-635A-185  
 ; Sequence 185, Application US/10125635A  
 ; Publication No. US20030039635A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Carter, Darrick D.  
 ; APPLICANT: Cheever, Martin A.  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Sutherland, R. Alec  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
 ; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
 ; FILE REFERENCE: 210121.465C7  
 ; CURRENT APPLICATION NUMBER: US/10/125,635A  
 ; CURRENT FILING DATE: 2002-07-19  
 ; NUMBER OF SEQ ID NOS: 461  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 185  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 US-10-125-635A-185



Query Match 100.0%; Score 51; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMPNAPYL 9  
|||  
Db 1 RMPNAPYL 9

Search completed: January 21, 2004, 08:57:41  
Job time : 32 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 21, 2004, 08:50:15 ; Search time 22 Seconds  
(without alignments)  
17.309 Million cell updates/sec

Title: US-09-625-963A-1

Perfect score: 51

Sequence: 1 RMFPNAPYL 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 77717

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/aa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/aa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/aa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/aa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/aa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	56.9	9	4	US-09-492-543-158
2	28	54.9	9	3	US-09-162-368B-26
3	28	54.9	9	3	US-09-161-877B-26
4	27	52.9	8	2	US-08-737-085A-6
5	27	52.9	8	3	US-09-246-258-6
6	27	52.9	8	3	US-09-532-106-6
7	27	52.9	8	4	US-09-839-666-6
8	26	51.0	6	2	US-08-672-805-12
9	26	51.0	8	3	US-08-540-922D-8
10	25	49.0	8	5	PCT-US94-03744-6
11	25	49.0	8	3	US-09-162-368B-28
12	25	49.0	7	1	US-09-161-877B-28
13	24	47.1	9	3	US-08-261-525A-6
14	24	47.1	7	4	US-09-367-940A-1
15	24	47.1	9	2	US-08-417-174-13
16	24	47.1	9	2	US-08-231-565A-13
17	24	47.1	9	2	US-09-007-961-13
18	24	47.1	9	3	US-08-159-339A-793
19	24	47.1	9	3	US-09-162-368B-24
20	24	47.1	9	3	US-09-161-877B-24
21	24	47.1	9	3	US-08-786-455B-5
22	24	47.1	9	3	US-09-267-439-12
23	24	47.1	9	4	US-09-311-784A-198
24	24	47.1	9	4	US-09-073-138-13
25	23	45.1	7	6	5514590-12
26	23	45.1	8	2	US-08-177-109A-24
27	23	45.1	8	2	US-08-687-706-24

28	23	45.1	8	3	US-08-444-818-433	Sequence 433, App
29	23	45.1	8	3	US-08-444-818-434	Sequence 434, App
30	23	45.1	8	5	PCT-US94-01321-70	Sequence 70, App
31	22	43.1	6	2	US-08-672-805-11	Sequence 11, App
32	22	43.1	7	4	US-09-461-325-321	Sequence 321, App
33	22	43.1	8	3	US-09-484-318-7	Sequence 7, App
34	22	43.1	8	3	US-09-484-319-7	Sequence 7, App
35	22	43.1	8	3	US-09-484-320-7	Sequence 7, App
36	22	43.1	8	3	US-09-484-321-7	Sequence 7, App
37	22	43.1	8	3	US-09-484-323-7	Sequence 7, App
38	22	43.1	8	3	US-09-325-769-8	Sequence 8, App
39	22	43.1	8	3	US-09-636-170-7	Sequence 7, App
40	22	43.1	8	3	US-09-637-518-7	Sequence 7, App
41	22	43.1	8	4	US-09-757-933B-8	Sequence 8, App
42	22	43.1	9	3	US-09-162-368B-25	Sequence 25, App
43	22	43.1	9	3	US-09-161-877B-25	Sequence 25, App
44	22	43.1	9	4	US-09-492-543-180	Sequence 180, App
45	22	43.1	9	4	US-09-461-325-386	Sequence 386, App

## ALIGNMENTS

```
RESULT 1
US-09-492-543-158
Sequence 158, Application US/09492543A
Patent No. 6316213
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
FILE REFERENCE: D6223CIP-B
CURRENT APPLICATION NUMBER: US/09/492,543A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 09/039,211
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 189
SOFTWARE: WORD 6.0.1 for Macintosh
SEQ ID NO 158
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Residues 96-104 of the PUMP-1 protein
US-09-492-543-158

Query Match 56.9%; Score 29; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 MFNPAP 7
DB 2 LFNPSP 7

RESULT 2
US-09-162-368B-26
Sequence 26, Application US/09162368B
Patent No. 6083703
GENERAL INFORMATION:
APPLICANT: WANG, R.F.; ROSENBERG, S. A.
TITLE OF INVENTION: IDENTIFICATION OF TRP-2 AS
TITLE OF INVENTION: A HUMAN TUMOR ANTIGEN RECOGNIZED BY CYTOTOXIC T
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
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MEDIUM TYPE: FLOPPY DISK.  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MICROSOFT WORD 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/162,368B  
FILING DATE: 28-SEPT-1998  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/725,736  
FILING DATE: 04-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/599,602  
FILING DATE: 09-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: KATHRYN M. BROWN  
REGISTRATION NUMBER: 34,556  
REFERENCE/DOCKET NUMBER: 2026-4243US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO ACID  
STRANDEDNESS: UNKNOWN  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: PEPTIDE  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-09-162-368B-26

Query Match 54.9%; Score 28; DB 3; Length 9;  
Best Local Similarity 57.1%; Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 MFNPAPY 8  
DB 2 LFPGRPY 8  
RESULT 3  
US-09-161-877B-26  
Sequence 26, Application US/09161877B  
Patent No. 6132980  
GENERAL INFORMATION:  
APPLICANT: WANG, R.F.; ROSENBERG, S. A.  
TITLE OF INVENTION: IDENTIFICATION OF TRP-2  
TITLE OF INVENTION: AS A HUMAN TUMOR ANTIGEN RECOGNIZED BY  
TITLE OF INVENTION: CYTOTOXIC T LYMPHOCYTES  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MICROSOFT WORD 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/161,877B  
FILING DATE: 28-SEPT-1998  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/725,736  
FILING DATE: 04-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/599,602  
FILING DATE: 09-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: KATHRYN M. BROWN  
REGISTRATION NUMBER: 34,556  
REFERENCE/DOCKET NUMBER: 2026-4243US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO ACID  
STRANDEDNESS: UNKNOWN  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: PEPTIDE  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-09-161-877B-26

Query Match 54.9%; Score 28; DB 3; Length 9;  
Best Local Similarity 57.1%; Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 MFNPAPY 8  
DB 2 LFPGRPY 8  
RESULT 4  
US-08-737-085A-6  
Sequence 6, Application US/08737085A  
Patent No. 5869232  
GENERAL INFORMATION:  
APPLICANT: SALBERG, MATTI  
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY  
TITLE OF INVENTION: EXCHANGER  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DARBY & DARBY PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/737,085A  
FILING DATE: 27-DEC-1996  
CLASSIFICATION: 426  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Green, Reza  
REGISTRATION NUMBER: 38,475  
REFERENCE/DOCKET NUMBER: 3846/0C569  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7659  
TELEFAX: 212-753-6237  
TELEX: 236687

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-737-085A-6

Query Match 52.9%; Score 27; DB 2; Length 8;  
Best Local Similarity 83.3%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PNAFYL 9  
Db 2 PNAFYL 7

RESULT 5  
US-09-246-258-6

Sequence 6, Application US/09246258  
Patent No. 6040137  
GENERAL INFORMATION:  
APPLICANT: SALLBERG, MATTI  
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY  
TITLE OF INVENTION: EXCHANGER  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DARBY & DARBY PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/246.258  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/737,085  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Green, Reza  
REGISTRATION NUMBER: 38,475  
REFERENCE/DOCKET NUMBER: 3846/0C569  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7659  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-246-258-6

Query Match 52.9%; Score 27; DB 3; Length 8;  
Best Local Similarity 83.3%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PNAFYL 9  
Db 2 PNAFYL 7

RESULT 6

US-09-532-106-6

Sequence 6, Application US/09532106  
Patent No. 6245895  
GENERAL INFORMATION:  
APPLICANT: SALLBERG, MATTI  
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY  
TITLE OF INVENTION: EXCHANGER  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DARBY & DARBY PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/532.106  
FILING DATE: 21-Mar-2000

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/737,085A  
FILING DATE: 27-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Green, Reza  
REGISTRATION NUMBER: 38,475  
REFERENCE/DOCKET NUMBER: 3846/0C569

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7659  
TELEFAX: 212-753-6237  
TELEX: 236687

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-532-106-6

Query Match 52.9%; Score 27; DB 3; Length 8;  
Best Local Similarity 83.3%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PNAFYL 9  
Db 2 PNAFYL 7

RESULT 7  
US-09-839-666-6

Sequence 6, Application US/09839666  
Patent No. 6469143

GENERAL INFORMATION:  
APPLICANT: SALLBERG, MATTI

TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY  
TITLE OF INVENTION: EXCHANGER  
NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:  
ADDRESSEE: DARBY & DARBY PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/839,666  
FILING DATE: 19-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/737,085  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Green, Reza  
REGISTRATION NUMBER: 38,475  
REFERENCE/DOCKET NUMBER: 3846/0C569  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7659  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-839-666-6  
Query Match 52.9%; Score 27; DB 4; Length 8;  
Best Local Similarity 83.3%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 PNAAYL 9  
DB 2 PNAAYL 7  
RESULT 8  
US-08-672-805-12  
Sequence 12, Application US/08672805  
Patent No. 5831003  
GENERAL INFORMATION:  
APPLICANT: Baumbach, George A.,  
APPLICANT: Buettner, Joseph A.,  
APPLICANT: Dadd, Christopher A.,  
APPLICANT: Hammond, David J.,  
TITLE OF INVENTION: Peptides which Bind to Prothrombin and  
NUMBER OF INVENTION: Thrombin  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bayer Corporation  
STREET: 800 Dwight Way  
STREET: P. O. Box 1986  
CITY: Berkeley  
STATE: California  
COUNTRY: USA  
ZIP: 94701-1986  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB Storage  
COMPUTER: IBM  
OPERATING SYSTEM: DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/672,805  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Giblin, James A.,  
REGISTRATION NUMBER: 25772  
REFERENCE/DOCKET NUMBER: MSB-7236  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510)705-7910

TELEFAX: (510)705-7904  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6  
TYPE: amino acid  
STRANDEDNESS: single strand  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: peptide  
US-08-672-805-12  
Query Match 51.0%; Score 26; DB 2; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 PNAAYL 9  
DB 1 PFAAYL 6  
RESULT 9  
US-08-540-922D-8  
Sequence 8, Application US/08540922D  
Patent No. 6284476  
GENERAL INFORMATION:  
APPLICANT: Boon-Fallieur, Thierry; Brichard, Vincent; Van  
APPLICANT: Pel, Aline; De Plaen, Etienne; Coulie, Pierre;  
APPLICANT: Renaud Jean-Christophe; Wollet, Thomas; and  
APPLICANT: Lethe, Bernard.  
TITLE OF INVENTION: METHOD OF IDENTIFYING INDIVIDUALS SUFFERING  
TITLE OF INVENTION: FROM A CELLULAR ABNORMALITY SOME OF WHOSE  
TITLE OF INVENTION: ABNORMAL CELLS PRESENT COMPLEXES OF HUMAN  
TITLE OF INVENTION: LEUCOCYTE ANTIGEN TYROSINASE DERIVED  
TITLE OF INVENTION: PEPTIDES, AND METHODS FOR TREATING SAID  
TITLE OF INVENTION: INDIVIDUALS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felte & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WordPerfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/540,922D  
FILING DATE: October 11, 1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/054,714  
FILING DATE: 28 April 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/994,928  
FILING DATE: 22 December 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Mary Anne Schofield  
REGISTRATION NUMBER: 36,669  
REFERENCE/DOCKET NUMBER: LUD 5299.5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 836-3884  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8  
TYPE: amino acids  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: Protein

FEATURE:  
OTHER INFORMATION: SEQ of aa corresponding to nt 1816-1839  
OTHER INFORMATION: nt of SEQ ID NO: 1  
US-08-540-922D-8

Query Match 51.0%; Score 26; DB 3; Length 8;  
Best Local Similarity 57.1%; Pred. No. 2.5e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PNNAPYL 9  
|||  
Db 2 FPLSPYV 8

RESULT 10  
PCT-US94-03744-6  
Sequence 6, Application PC/TUS9403744  
GENERAL INFORMATION:  
APPLICANT: PETRI, WILLIAM A.  
APPLICANT: MCCOY, BARBARA J.  
APPLICANT: MANN, BARBARA J.  
TITLE OF INVENTION: 35/31 KDA SUBUNIT OF THE  
TITLE OF INVENTION: ENTAMOEBA  
TITLE OF INVENTION: HISTOLYTICA ADHERENCE LECTIN  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morlison & Foerster  
STREET: 2000 Pennsylvania Avenue, Suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/03744  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,679  
FILING DATE: 09-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 29148-20005.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US94-03744-6

Query Match 49.0%; Score 25; DB 5; Length 8;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PNNAPYL 8  
|||  
Db 3 PNNAPYL 7

RESULT 11  
US-09-162-368B-28  
Sequence 28, Application US/09162368B  
Patent No. 6083703

GENERAL INFORMATION:  
APPLICANT: WANG, R.F.; ROSENBERG, S. A.  
TITLE OF INVENTION: IDENTIFICATION OF TRP-2 AS  
TITLE OF INVENTION: A HUMAN TUMOR ANTIGEN RECOGNIZED BY CYTOTOXIC T  
TITLE OF INVENTION: LYMPHOCYTES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MICROSOFT WORD 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/162,368B  
FILING DATE: 28-SEPT-1998  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/725,736  
FILING DATE: 04-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/599,602  
FILING DATE: 09-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: KATHRYN M. BROWN  
REGISTRATION NUMBER: 34,556  
REFERENCE/DOCKET NUMBER: 2026-4243US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 751-6849  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO ACID  
STRANDEDNESS: UNKNOWN  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: PEPTIDE  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-09-162-368B-28

Query Match 49.0%; Score 25; DB 3; Length 9;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PNNAPYL 8  
|||  
Db 4 PNNAPYL 8

RESULT 12  
US-09-161-877B-28  
Sequence 28, Application US/09161877B  
Patent No. 6132980  
GENERAL INFORMATION:  
APPLICANT: WANG, R.F.; ROSENBERG, S. A.  
TITLE OF INVENTION: IDENTIFICATION OF TRP-2  
TITLE OF INVENTION: AS A HUMAN TUMOR ANTIGEN RECOGNIZED BY  
TITLE OF INVENTION: CYTOTOXIC T LYMPHOCYTES  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE

CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MICROSOFT WORD 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/161,877B  
FILING DATE: 28-SEPT-1998  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/725,736  
FILING DATE: 04-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/599,602  
FILING DATE: 09-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: KATHRYN M. BROWN  
REGISTRATION NUMBER: 34,556  
REFERENCE/DOCKET NUMBER: 2026-4243US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO ACID  
STRANDEDNESS: UNKNOWN  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: PEPTIDE  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-09-161-877B-28

Query Match 49.0%; Score 25; DB 3; Length 9;  
Best Local Similarity 80.0%; Pred. NO. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PNAPY 8  
4 PGAPY 8  
Db

RESULT 13  
US-08-261-525A-6  
Sequence 6, Application US/08261525A  
Patent No. 5569598  
GENERAL INFORMATION:  
APPLICANT: PARK, Soon Jae  
APPLICANT: LEE, Young Mee  
APPLICANT: WON, Teug Yeon  
APPLICANT: KWON, Soon Chang  
APPLICANT: LEE, Seung Joo  
APPLICANT: KIM, Jung Ho  
APPLICANT: KIM, Bum Joon  
TITLE OF INVENTION: NOVEL AMINOPEPTIDASE, PROCESSES FOR  
TITLE OF INVENTION: THE PREPARATION OF AMINOPEPTIDASE AND  
TITLE OF INVENTION: PROTEIN THEREFROM  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PARK, Soon Jae  
STREET: Lucky Apt. 6-101, Doryong-dong, Yuseong-gu  
CITY: Daejeon  
STATE: Daejeon  
COUNTRY: Republic of Korea

ZIP: 305-340  
ADDRESSEE: LEE, Young Mee  
STREET: Shinsung Apt. 3-306, 28-4, Nae-dong, Seo-gu  
CITY: Daejeon  
STATE: Daejeon  
COUNTRY: Republic of Korea  
ZIP: 302-181  
ADDRESSEE: WON, Teug Yeon  
STREET: Gongjak Hanyang Apt. 3-1201, 835,  
STREET: Tanbang-dong, Seo-gu  
CITY: Daejeon  
STATE: Daejeon  
COUNTRY: Republic of Korea  
ZIP: 302-223  
ADDRESSEE: KWON, Soon Chang  
STREET: Shinsung Apt. 3-107, 28-4, Nae-dong, Seo-gu  
CITY: Daejeon  
STATE: Daejeon  
COUNTRY: Republic of Korea  
ZIP: 302-181  
ADDRESSEE: LEE, Seung Joo  
STREET: Lucky Apt. B-107, 386-4, Doryong-dong,  
STREET: Yuseong-gu  
CITY: Daejeon  
STATE: Daejeon  
COUNTRY: Republic of Korea  
ZIP: 305-340  
ADDRESSEE: KIM, Jung Ho  
STREET: Lucky Dormitory 511, 386-1, Doryong-dong,  
STREET: Yuseong-gu  
CITY: Daejeon  
STATE: Daejeon  
COUNTRY: Republic of Korea  
ZIP: 305-340  
ADDRESSEE: KIM, Bum Joon  
STREET: Lucky Dormitory 502, 386-1, Doryong-dong,  
STREET: Yuseong-gu  
CITY: Daejeon  
STATE: Daejeon  
COUNTRY: Republic of Korea  
ZIP: 305-340  
COUNTRY: Republic of Korea  
CITY: Daejeon  
STATE: Daejeon  
COUNTRY: Republic of Korea  
ZIP: 305-340  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk, 3.5 inch, 1.44MB storage  
COMPUTER: IBM PC/AT  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/261,525A  
FILING DATE: 17-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: KR 93-11107  
FILING DATE: 17-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Shahan Isalam  
REGISTRATION NUMBER: 32,507  
REFERENCE/DOCKET NUMBER: A-9883  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-1000  
TELEFAX: (212) 953-7249  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-261-525A-6

Query Match 47.1%; Score 24; DB 1; Length 7;  
Best Local Similarity 66.7%; Pred. NO. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 MPNAP 7



Db 1 MFPTP 6

## RESULT 14

US-09-367-940A-1  
Sequence 1, Application US/09367940A  
Patent No. 6428997

## GENERAL INFORMATION:

APPLICANT: LG CHEMICAL LTD.

LEE, Young-Phil

HAN, Kyuboem

PARK, Soon-Jae

LEE, Seung-Joo

TITLE OF INVENTION: Aminopeptidase  
derived from Bacillus licheniformis  
and process for preparation of natural  
type proteins

## NUMBER OF SEQUENCES: 4

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: BACHMAN & LAPOINTE, P.C.

STREET: Suite 1201, 900 Chapel Street

CITY: New Haven

STATE: Connecticut

COUNTRY: U.S.A.

ZIP: 06510-2802

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage

COMPUTER: IBM

OPERATING SYSTEM: WINDOWS 95/98

## SOFTWARE: MS WORD

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/367,940A

FILING DATE: 18-Aug-1999

INFORMATION FOR SEQ ID NO: 1:

## SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1

US-09-367-940A-1

Query Match 47.1%; Score 24; DB 4; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 MFPTP 7  
Db 1 MFPTP 6

## RESULT 15

US-08-417-174-13

Sequence 13, Application US/08417174

Patent No. 5844075

## GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

TITLE OF INVENTION: MELANOMA ANTIGENS AND

TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

NUMBER OF SEQUENCES: 126

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: MORGAN & PINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

## COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 13:

## SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

US-08-417-174-13

Query Match 47.1%; Score 24; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PNP 7  
Db 4 PNP 7

Search completed: January 21, 2004, 08:53:24  
Job time : 23 secs

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